

GenCore version 5.1.4_p5_4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:56:07 ; Search time 44 Seconds

(without alignments)
292.773 Million cell updates/sec

Title: US-09-142-524D-3

Perfect score: 711
Sequence: 1 MKVTVAFNFGNGRNRVFIKR.....KFIRRVGGIIAAYQNPASWK 134

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	188	26.4	374	2 JC2124	major allergen Cry
2	188	26.4	374	2 JC2123	major allergen Cry
3	148.5	20.9	514	2 S48730	Cry j II protein -
4	148.5	20.9	514	2 JC2498	second major aller
5	118.5	16.7	514	2 JC7100	polygalacturonase
6	110.5	15.5	542	2 T06728	pectate lyase (EC
7	107.5	15.1	507	2 JC7366	Jun a 2 protein -
8	104.5	14.7	463	2 T46165	pectate lyase-like
9	103	14.5	404	2 S12209	pectate lyase (EC
10	99	13.9	472	2 T51456	pectate lyase-like
11	98.5	13.9	396	2 A39099	allergen Amb a 1.1
12	97	13.6	397	2 C53240	allergen Amb a 1.3
13	97	13.6	397	2 C39099	allergen Amb a 1.3
14	97	13.6	455	2 T00856	pectate lyase (EC
15	95.5	13.4	459	2 G86278	hypothetical prote
16	94.5	13.3	404	2 T05556	pectate lyase (EC
17	94.5	13.3	431	2 F86179	hypothetical prote
18	93	13.1	397	2 S26211	pectate lyase (EC
19	93	13.1	398	2 B39099	allergen Amb a 1.2
20	93	13.1	397	2 T09524	allergen Amb a 1.2
21	92	12.9	450	2 E53240	allergen Amb a 1.1
22	92	12.9	398	2 B53240	allergen Amb a 1.2
23	91.5	12.9	368	2 C86427	probable pectate 1
24	91	12.8	398	2 T07058	pectate lyase (EC
25	89	12.5	392	2 D53240	allergen Amb a 1.4
26	89	12.5	434	2 S29612	pectate lyase (EC
27	88	12.4	438	2 S43335	pectate lyase (EC
28	84	11.8	374	2 T05240	pectate lyase (EC
29	84	11.8	374	2 H85148	probable pectate 1

30	84	11.8	390	2 H86253	hypothetical prote
31	84	11.8	394	2 T49115	pectate lyase like
32	82.5	11.6	449	2 S27098	pectate lyase (EC
33	82	11.5	394	2 T49116	pectate lyase like
34	81	11.4	219	2 C84647	probable synaptobr
35	79	11.1	274	2 T03932	pectate lyase (EC
36	78.5	11.0	418	2 T07701	pectate lyase (EC
37	78	11.0	341	2 T47653	pectate lyase-like
38	76.5	10.8	648	2 S10869	enterotoxin A - C1
39	76	10.7	398	2 F72335	hypothetical prote
40	74.5	10.5	368	2 F83785	required for glyco
41	74	10.4	219	2 T04630	synaptobrevin homo
42	71.5	10.1	657	2 T22451	hypothetical prote
43	71	10.0	2710	2 A37052	toxins A - Clostrid
44	70.5	9.9	622	2 S17402	paraspore crystal
45	70.5	9.9	1003	2 T26746	hypothetical prote

ALIGNMENTS

RESULT 1

JC2124 major allergen Cry j I precursor (clone pCCI-15) - Japanese cedar

C:Species: Cryptomeria japonica (Japanese cedar)

C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 21-Jul-2000

C:Accession: JC2124

R:Some, T.; Komiyama, N.; Shimizu, K.; Kusakabe, T.; Morikubo, K.; Kino, K.

Biochem. Biophys. Res. Commun. 199, 619-625, 1994

A:Title: Cloning and sequencing of cDNA coding for Cry j I, a major allergen of Japanese

A:Reference number: JC2123; MUID:94183234; PMID:8135802

A:Accession: JC2124

A:Molecule type: mRNA

A:Residues: 1-374 <SON>

A:Cross-references: GB:D26545; NID:9493633; PIDN:BAA05543.1; PID:9493634

A:Experimental source: pollen

A>Note: the authors described carbohydrate binding site for residue 279

C:Superfamily: pectate lyase LAR59

C:Keywords: glycoprotein; pollen

P.1-21/Domain: signal sequence #status predicted <SIG>

F.122-374/Product: major allergen Cry j I (clone pCCI-15) #status predicted <MAT>

F.158,191,293,354/Binding site: carbohydrate (asn) (covalent) #status predicted

Query Match 26.4%; Score 188; DB 2; Length 374;

Best Local Similarity 71.2%; Pred. No. 1.9e-12;

Matches 37; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 73 RPLWTFSGNNMNTKMKMPYTAGYKTPDGRRAVSYYVHNGAKFIRRVGGII 124

DB 87 RPLWTFSGNNMNTKMKMPYTAGYKTPDGRRAVSYYVHNGAKFIRRVGGII 138

RESULT 2

JC2123 major allergen Cry j I precursor (clone pCCI-2-2) - Japanese cedar

C:Species: Cryptomeria japonica (Japanese cedar)

C:Date: 14-Jul-1994 #sequence_revision 14-Jul-1994 #text_change 21-Jul-2000

C:Accession: JC2123; PC2065

R:Some, T.; Komiyama, N.; Shimizu, K.; Kusakabe, T.; Morikubo, K.; Kino, K.

Biochem. Biophys. Res. Commun. 199, 619-625, 1994

A:Title: Cloning and sequencing of cDNA coding for Cry j I, a major allergen of Japanese

A:Reference number: JC2123; MUID:94183234; PMID:8135802

A:Accession: JC2123

A:Molecule type: mRNA

A:Residues: 1-374 <SON>

A:Cross-references: GB:D26544; NID:9493631; PIDN:BAA05542.1; PID:9493632

A:Experimental source: pollen

A:Accession: PC2065

A:Molecule type: protein

A:Residues: 22-53;58-81;219-232;236-258;299-307;346-372 <SO2>

A>Note: the authors described carbohydrate binding site for residue 279

C:Superfamily: pectate lyase LAR59

C:Keywords: glycoprotein; pollen

F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-374/Product: major allergen Cry j I (clone pCCI-2-2) #status predicted <MAT>
F:158,191,293,354/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match

Best Local Similarity 26.4%; Score 188; DB 2; Length 374;
Matches 37; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 73 RPLMIIFSGNNMIKLMKMPYIAGYTFDGRRAVSYYHVNGAKFIRVDGI 124
DB 87 RPLMIIFSGNNMIKLMKMPYIAGYTFDGRRAVSYYHVNGAKFIRVDGI 138

RESULT 3

S48730
Cry j II protein - Japanese cedar
C:Species: Cryptomeria japonica (Japanese cedar)
C:Date: 07-May-1995 #sequence_revision 21-Jul-1995 #text_change 28-May-1999
C:Accession: S48730
R:Kanda, M.; Kurose, M.; Torigoe, K.; Hino, K.; Taniguchi, Y.; Fukuda, S.; Usui, M.; Kurose Letc. 353, 124-128, 1994
A:Title: Molecular cloning of the second major allergen, Cry j II, from Japanese cedar
A:Reference number: S48730; MUID:95010777; PMID:7926035
A:Accession: S48730
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-514 <NAM>
A:Cross-references: GB:D37765; NID:9577695; PIDN:BA007021.1; PID:d1007598; PID:9577696

Query Match

Best Local Similarity 20.9%; Score 148.5; DB 2; Length 514;
Matches 41; Conservative 8; Mismatches 21; Indels 29; Gaps 2;

QY 31 IDIFASKNFHLQXNTTIGTRRMKNRIMWQFAKLTGFTLMGRPLMIIFSGNNMIKLMKMP 90
DB 236 IDIFASKNFHLQXNTTIGT-----DDCVALTGSSNVIHDL 272

QY 91 MYIAGYKTFD-----RAEVSYYHVNGAKFIRVDGI 123
DB 273 ICGPHGISISLGRNSRAVSYYHVNGAKFIRVDGI 311

RESULT 4

JC2498
second major allergen Cry j II precursor - Japanese cedar
C:Species: Cryptomeria japonica (Japanese cedar)
C:Date: 16-Mar-1995 #sequence_revision 26-May-1995 #text_change 21-Jul-2000
C:Accession: JC2498; PC2346; A60147
R:Komiyama, N.; Sone, T.; Shimizu, K.; Morikubo, K.; Kino, K.
Biochem. Biophys. Res. Commun. 201, 1021-1028, 1994
A:Title: cDNA cloning and expression of Cry j II, the second major allergen of Japanese
A:Reference number: JC2498; MUID:94271186; PMID:8002972
A:Accession: JC2498
A:Molecule type: mRNA
A:Residues: 1-514 <KOM>
A:Cross-references: DDBJ:D29772; NID:9506857; PIDN:BA006172.1; PID:9506858
A:Accession: PC2346

A:Molecule type: protein
A:Residues: 52-61 <KO2>
R:Sakaguchi, M.; Inouye, S.; Taniai, M.; Ando, S.; Usui, M.; Matuhasi, T.
Allergy 45, 309-312, 1990
A:Title: Identification of the second major allergen of Japanese cedar pollen.
A:Reference number: A60147; MUID:90342988; PMID:2382797
A:Accession: A60147

A:Molecule type: protein
A:Residues: 55-64 <SAK>
C:Keywords: glycoprotein, pollen
F:1-54/Domain: signal sequence #status predicted <SIG>
F:55-460/Product: second major allergen Cry j #status predicted <MAT>
F:429,460,472/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 20.9%; Score 148.5; DB 2; Length 514;
Best Local Similarity 41.4%; Pred. No. 4.9e-08;

5

Matches 41; Conservative 8; Mismatches 21; Indels 29; Gaps 2;

QY 31 IDIFASKNFHLQXNTTIGTRRMKNRIMWQFAKLTGFTLMGRPLMIIFSGNNMIKLMKMP 90
DB 236 IDIFASKNFHLQXNTTIGT-----DDCVALTGSSNVIHDL 272

QY 91 MYIAGYKTFD-----RAEVSYYHVNGAKFIRVDGI 123
DB 273 ICGPHGISISLGRNSRAVSYYHVNGAKFIRVDGI 311

RESULT 5

JC7100
polygalacturonase Cha o 2 - Japanese cypress
C:Species: Chamaecyparis obtusa (Japanese cypress)
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 11-May-2000
C:Accession: JC7100; PC7026
R:Mori, T.; Yokoyama, M.; Komiyama, N.; Okano, M.; Kino, K.
Biochem. Biophys. Res. Commun. 263, 166-171, 1999
A:Title: Purification, identification, and cDNA cloning of Cha o 2, the second major all
A:Reference number: JC7100; MUID:99417540; PMID:10486272
A:Accession: JC7100
A:Molecule type: mRNA
A:Residues: 1-514 <MOR>
A:Accession: PC7026
A:Molecule type: protein
A:Residues: 51-62 <MO2>

Query Match 16.7%; Score 118.5; DB 2; Length 514;
Best Local Similarity 35.4%; Pred. No. 8.3e-05;
Matches 35; Conservative 10; Mismatches 25; Indels 29; Gaps 2;

QY 31 IDIFASKNFHLQXNTTIGTRRMKNRIMWQFAKLTGFTLMGRPLMIIFSGNNMIKLMKMP 90
DB 236 IDIFASKNFHLQXNTTIGT-----DDCVALTGSSNVIHDL 272

QY 91 MYIAGYKTF-----DGRRAVSYYHVNGAKFIRVDGI 123
DB 273 ICGPHGISISLGRNSRAVSYYHVNGAKFIRVDGI 311

RESULT 6

T06728
pectate lyase (EC 4.2.2.2) F28P10.100 - Arabidopsis thaliana
N:Alternate names: pectate lyase F28P10.100
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 23-Jul-1999
C:Accession: T06728
R:Queletier, F.; Choisey, N.; Robert, C.; Brothier, P.; Wincker, P.; Catolico, L.; Artigau
submitted to the Protein Sequence Database, April 1999
A:Reference number: 215793
A:Accession: T06728
A:Molecule type: DNA

A:Residues: 1-542 <QUE>
A:Cross-references: EMBL:AL049655
A:Experimental source: cultivar Columbia; BAC clone F28P10
C:Genetics:
A:Map position: 3
A:Introns: 46/2; 346/3; 413/2; 480/2
A:Notes: F28P10.100
C:Superfamily: pectate lyase LNT59
C:Keywords: carbon-oxygen lyase

Query Match 15.5%; Score 110.5; DB 2; Length 542;
Best Local Similarity 43.3%; Pred. No. 0.00064;
Matches 26; Conservative 9; Mismatches 20; Indels 5; Gaps 2;

QY 67 FTLMGRPLMIIFSGNNMIKLMKMPYIAGYTFDGRRAVSYYHV--NGAKFIRVDGI 124
DB 139 YGVIOEPLMIIFSGNNMIKLMKMPYIAGYTFDGRRAVSYYHV--NGAKFIRVDGI 195

RESULT 7

A:Residues: 1-396 <RAF>
 A:Cross-references: GB:M63116
 R:Smith, J.J.; Olson, J.R.; Klapper, D.G.
 Mol. Immunol. 25, 355-365, 1988
 A:Title: Monoclonal antibodies to denatured ragweed pollen allergen Amb a I: characterization
 A:Reference number: A60895; MUID:88288254; PMID:2456454
 A:Accession: A60895
 A:Molecule type: Protein
 A:Residues: 256-273;292-303, 'W', 305-306 <SMI>
 R:Griffith, I.J.; Pollock, J.; Klapper, D.G.; Rogers, B.L.; Nault, A.K.
 Int. Arch. Allergy Appl. Immunol. 96, 296-304, 1991
 A:Title: Sequence polymorphism of Amb a I and Amb a II, the major allergens in Ambrosia
 A:Reference number: A53240; MUID:92234570; PMID:1809687
 A:Accession: A53240
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-396 <GRI>
 A:Cross-references: GB:M80558; NID:9166434; PIDN:AAA32665.1; PID:9166435
 C:Superfamily: pectate lyase LAT59
 C:Keywords: glycoprotein; pollen
 F:36/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 13.6%; Score 97; DB 2; Length 396;
 Best Local Similarity 34.7%; Pred. No. 0.0087;
 Matches 26; Conservative 12; Mismatches 22; Indels 15; Gaps 3;

Query 73 RPLMTIFSGNMNITKMKPMYIAGYKTFDGRRAEVSIVH-----VNGAK-FIRVD----- 121
 Db 113 RPLMTIFSRMVRILDKEMVWNSDKTIDGAKVEIINAGFTLNGVKNVIHNNIMHDVK 172

Query 122 ----GIIAAYNPAS 132
 Db 173 VNPGLIKSNDGPA 187

RESULT 12
 CS3240
 allergen Amb a I.3 precursor - common ragweed
 C:Species: Ambrosia artemisiifolia (common ragweed)
 C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 18-Sep-1998
 C:Accession: CS3240
 R:Griffith, I.J.; Pollock, J.; Klapper, D.G.; Rogers, B.L.; Nault, A.K.
 Int. Arch. Allergy Appl. Immunol. 96, 296-304, 1991
 A:Title: Sequence polymorphism of Amb a I and Amb a II, the major allergens in Ambrosia
 A:Reference number: A53240; MUID:92234570; PMID:1809687
 A:Accession: CS3240
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-397 <GRI>
 A:Cross-references: GB:M80560
 C:Superfamily: pectate lyase LAT59
 C:Keywords: pollen

Query Match 13.6%; Score 97; DB 2; Length 397;
 Best Local Similarity 29.5%; Pred. No. 0.013;
 Matches 31; Conservative 7; Mismatches 33; Indels 34; Gaps 3;

Query 52 WKNNRIWLO-----FAKLT-----GFTLMGRRLPMIIF 79
 Db 61 WENNROALADCAQGFAGKGYGKMGDVYTVTSNLDVDPANPKEGTLRFAPAAQNRPLMIIF 120

Query 80 SGNNITKMKPMYIAGYKTFDGRRAEVSIVHNGAKFIRVDGII 124
 Db 121 KNDMVINLQELVNSDKTIDGRGVKEI--INGGLTLMNVKNII 163

RESULT 13
 C39099
 allergen Amb a I.3 - common ragweed
 C:Species: Ambrosia artemisiifolia (common ragweed)
 C:Date: 27-Nov-1991 #sequence_revision 03-Apr-1992 #text_change 29-Sep-1999
 C:Accession: C39099

R:Rafnar, T.; Griffith, I.J.; Kuo, M.; Bond, J.F.; Rogers, B.L.; Klapper, D.G.
 J. Biol. Chem. 266, 1229-1236, 1991
 A:Title: Cloning of Amb a I (antigen E), the major allergen family of short ragweed pol
 A:Reference number: A39099; MUID:91093235; PMID:1702434
 A:Accession: C39099
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-397 <RAF>
 A:Cross-references: GB:M62961; NID:9166440; PIDN:AAA32668.1; PID:9166441
 C:Superfamily: pectate lyase LAT59
 C:Keywords: pollen

Query Match 13.6%; Score 97; DB 2; Length 397;
 Best Local Similarity 29.5%; Pred. No. 0.013;
 Matches 31; Conservative 7; Mismatches 33; Indels 34; Gaps 3;

Query 52 WKNNRIWLO-----FAKLT-----GFTLMGRRLPMIIF 79
 Db 61 WENNROALADCAQGFAGKGYGKMGDVYTVTSNLDVDPANPKEGTLRFAPAAQNRPLMIIF 120

Query 80 SGNNITKMKPMYIAGYKTFDGRRAEVSIVHNGAKFIRVDGII 124
 Db 121 KNDMVINLQELVNSDKTIDGRGVKEI--INGGLTLMNVKNII 163

RESULT 14
 T00856
 pectate lyase (EC 4.2.2.2) T20F6.14 - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 02-Feb-2001
 C:Accession: T00856; A84440
 R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
 submitted to the EMBL data library, March 1998
 A:Description: Arabidopsis thaliana chromosome II BAC T20F6 genomic sequence.
 A:Reference number: Z14206
 A:Accession: T00856
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-455 <ROU>
 A:Cross-references: EMBL:AC002521; NID:92947056; PIDN:AAC05350.1; PID:92947069
 A:Experimental source: cultivar Columbia
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L.
 eus, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J
 Nature 402, 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: A84440
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-455 <STO>
 A:Cross-references: GB:AE002093; NID:92947069; PIDN:AAC05350.1; GSPDB:GNO0139
 C:Genetics:
 A:Gene: At2g02720
 A:Map position: 2
 A:Introns: 66/2; 295/3; 376/3
 A:Note: T20F6.14
 C:Superfamily: pectate lyase LAT59
 C:Keywords: carbon-oxygen lyase

Query Match 13.6%; Score 97; DB 2; Length 455;
 Best Local Similarity 46.2%; Pred. No. 0.015;
 Matches 24; Conservative 9; Mismatches 13; Indels 6; Gaps 3;

Query 73 RPLMTIFSGNMNITKMKPMYIAGYKTFDGRRAEVSIVHNGA---KFTRRV 120
 Db 166 RPLMTIFSRMIRKLOEHLITNDKTIIDGRGAKI-YI-TGAGALTQFVRNV 215

RESULT 15
 G86278
 hypothetical protein F14I7.19 (imported) - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)

C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 01-Mar-2002

C:Accession: G86278

R:Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Creasy, A.R.; Dewar, K.;
ansen, N.F.; Hughes, B.; Hulzar, L.

Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.

A:Reference number: A86141; MUID:21016719; PMID:11130712

A:Accession: G86278

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-459 <STO>

A:Cross-references: GB:AF005172; NID:G7262684; PIDN:AAF43942.1; GSPDB:GN00141

C:Genetics:

A:Map position: 1

C:Superfamily: pectate lyase LATS9

Query Match

Best Local Similarity 13.4%; Score 95.5; DB 2; length 459;

Matches 32; Conservative 9; Mismatches 28; Indels 43; Gaps 4;

QY 50 RRMKNNRIMLQFAKLTGFTL-MGR----- 73

DB 115 RNMANNR-----KKLDVCVGFGRRTTGKGPRIYVKDASDNDLINPKGTLRHAVTRD 169

QY 74 -PLMIFSGMNNIKLKMPIYAGYKTFDGRRAEVSYYVNGAKFIRRDGII 124

DB 170 GPLMIFPASMIIKLQDELMTSDKTIIDRGARY-YIMEGAGLTLPVNNVI 220

Search completed: May 5, 2003, 16:59:58

Job time : 55 secs

GenCore version 5.1.4.p5 4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:48:41 ; Search time 12 Seconds
(Without alignments)

463.152 Million cell updates/sec

Title: US-09-142-524D-3

Perfect score: 711

Sequence: 1 MKTVAFNNGPNRRVFIKR.....KPIRRVDGIIAAYQNPASWK 134

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 112892 seqs, 41476328 residues

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	188	26.4	374	1	SBP_CRYUA
2	150	21.1	367	1	MPAI_JUNAS
3	148.5	20.9	514	1	MPA2_CRYUA
4	143	20.1	346	1	MPAI_CUPAR
5	142	20.0	375	1	MPAI_CHA0B
6	103	14.5	404	1	9612_LYCRS
7	98.5	13.9	396	1	MP11_AMBAR
8	97	13.6	397	1	MP13_AMBAR
9	93	13.1	397	1	PEL_TOBAC
10	93	13.1	398	1	MP12_AMBAR
11	92	12.9	397	1	PE56_LYCRS
12	91	12.8	398	1	PE56_LYCRS
13	89	12.5	392	1	MP14_AMBAR
14	89	12.5	434	1	PEL_LILLO
15	82.5	11.6	449	1	PE59_LYCRS
16	81.5	11.5	234	1	A29B_DROME
17	80.5	11.3	605	1	PHAC_METEX
18	71	10.0	2710	1	TOXA_CLODI
19	70.5	9.9	622	1	C2AC_BACTU
20	69.5	9.8	338	1	YX8_YEAST
21	68.5	9.6	234	1	A29B_DROS1
22	68.5	9.6	551	1	CHIT_NPVAC
23	67.5	9.5	985	1	AGLU_ASPOR
24	67.5	9.5	1070	1	YHV4_YEAST
25	67	9.4	757	1	FIX1_RHIME
26	66.5	9.4	110	1	Y12K_SMSV4
27	66	9.3	375	1	Y4ED_RHISN
28	66	9.3	382	1	PHAT_BACSU
29	66	9.3	646	1	NODO_RHIS3
30	65	9.1	576	1	DPEP_SOLUTU
31	65	9.1	726	1	YB1D_SCHPO
32	65	9.1	781	1	TL22_CHICK
33	64.5	9.1	1010	1	CLPE_CHLEU

34	64	9.0	532	1	PUR2_ARATH	P52420 arabidopsis
35	64	9.0	633	1	NODO_RHISB	O07309 r nodg bifu
36	63.5	8.9	196	1	Y4O7_YEAST	O04487 saccharomyc
37	63.5	8.9	309	1	Y4O0_RHISN	P55602 rhizobium s
38	63.5	8.9	326	1	SCRR_PEDPE	P43472 pedicoccus
39	63	8.9	347	1	NIZM_RABIT	O79428 oryctolagus
40	63	8.9	477	1	GLGA_SYNY3	P74521 synechocyst
41	63	8.9	522	1	CEV1_ORENI	P70091 oreochromis
42	63	8.9	725	1	GUNG_CLOCE	P37700 clostridium
43	63	8.9	755	1	COMP_RAT	P35444 rattus norv
44	63	8.9	1121	1	WDR6_HUMAN	O9nmw5 homo sapien
45	62.5	8.8	262	1	FLG3_AGRTS	O44338 agrobacteri

ALIGNMENTS

RESULT 1	SBP_CRYUA	STANDARD;	PRT;	374 AA.
ID	SBP_CRYUA			
AC	P18632;			
DT	01-NOV-1990 (Rel. 16, Created)			
DT	01-NOV-1995 (Rel. 32, Last sequence update)			
DT	30-MAY-2000 (Rel. 39, Last annotation update)			
DE	Sugi basic protein precursor (SBP) (Major allergen Cry j 1) (Cry j I).			
OS	Cryptomeria japonica (Japanese cedar).			
OC	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;			
OC	Spermatophyta; Coniferales; Cupressaceae; Cryptomeria.			
NCBI_TaxID=3369;				
OK	NCBI_TaxID=3369;			
RN	[1]			
RP	SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.			
RC	TISSUE=Pollen;			
RX	MEDLINE=94183234; PubMed=8135802;			
RA	Sone T., Komiyama N., Shimizu K., Kusakabe T., Morikubo K.,			
RA	Kino K.,			
RT	"Cloning and sequencing of cDNA coding for Cry j I, a major allergen			
RT	of Japanese cedar pollen.";			
RL	Biochem. Biophys. Res. Commun. 199;619-625 (1994).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Pollen;			
RA	Namba M., Kurose M., Torigoe K., Fukuda S., Kurimoto M.,			
RL	Submitted (JUL-1994) to the EMBL/GenBank/DBD databases.			
RN	[3]			
RP	SEQUENCE OF 22-41.			
RC	TISSUE=Pollen;			
RX	MEDLINE=89031257; PubMed=3181436;			
RA	Tanai M., Ando S., Usui M., Kurimoto M., Sakaguchi M., Inoue S.,			
RA	Matsumoto T.,			
RT	"N-terminal amino acid sequence of a major allergen of Japanese cedar			
RT	pollen (Cry j I).";			
RL	FEBS Lett. 239;329-332 (1988).			
RN	[4]			
RP	CARBOHYDRATES.			
RC	TISSUE=Pollen;			
RX	MEDLINE=95003748; PubMed=7920021;			
RA	Hijikata A., Matsumoto I., Kojima K., Ogawa H.,			
RT	"Antigenicity of the oligosaccharide moiety of the Japanese cedar			
RT	(Cryptomeria japonica) pollen allergen, Cry j I."			
RL	Int. Arch. Allergy Immunol. 105;198-202 (1994).			
RN	[5]			
RP	STRUCTURE OF CARBOHYDRATES.			
RC	TISSUE=Pollen;			
RX	MEDLINE=95332249; PubMed=7608114;			
RA	Hino K., Yamamoto S., Sano O., Taniguchi Y., Kohno K., Usui M.,			
RA	Fukuda S., Hanawa H., Hanyama H., Kurimoto M.,			
RT	"Carbohydrate structures of the glycoprotein allergen Cry j I from			
RT	Japanese cedar (Cryptomeria japonica) pollen."			
RL	J. Biochem. 117;289-295 (1995).			
CC	-1- PPM: CONTAINS FUCOSE/XULOSE-CONTAINING N-LINKED OLIGOSACCHARIDES.			
CC	-1- DISEASE: THIS PROTEIN IS THE MAJOR ALLERGEN OF JAPANESE CEDAR			
CC	POLLEN. THE MOST COMMON POLLEN ALLERGEN IN JAPAN.			
CC	-1- MISCELLANEOUS: THE SEQUENCE OF CRY J I FORM A IS SHOWN HERE. FORM			

B DIFFERS IN SIX POSITIONS.
 CC SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
 CC AMB A I/AMB A II/CRY J I SUBFAMILY.
 CC
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DR EMBL; D26544; BAA05542.1; -
 DR EMBL; D26545; BAA05543.1; -
 DR EMBL; D34639; BAA07020.1; -
 DR PIR; A44773; A44773.
 DR GLYCOSULEDB; P18632; -
 DR InterPro; IPR002022; Amb_allergen.
 DR Pfam; PF00544; pec_lyase; 1.
 DR PRINTS; PR00807; AMBALLERGEN.
 KW Allergen; Glycoprotein; Multigene family; Signal.
 FT SIGNAL 1 21
 FT CHAIN 1 21
 FT CARBOHYD 158 158 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (COMPLEX).
 FT CARBOHYD 293 293 /FTID-CAR 000135.
 FT CARBOHYD 354 354 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 354 354 /FTID-CAR 000136.
 FT VARIANT 12 12 L -> F (IN CRY J 1-B).
 FT VARIANT 143 143 H -> Y (IN CRY J 1-B).
 FT VARIANT 202 202 S -> T (IN CRY J 1-B).
 FT VARIANT 221 221 L -> S (IN CRY J 1-B).
 FT VARIANT 358 358 O -> H (IN CRY J 1-B).
 FT VARIANT 361 361 K -> Q (IN CRY J 1-B).
 SQ SEQUENCE 374 AA; 40645 MW; 74AB25950248F56F CRC64;

Query Match 26.4%; Score 188; DB 1; Length 374;
 Best Local Similarity 71.2%; Pred. No. 2.7e-12;
 Matches 37; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 73 RPLMTIFSGNMNITKLMKPMYIAGYKTFDGRRAEVSVYHNGAKFRRVDGII 124
 DB 87 RPLMTIFSGNMNITKLMKPMYIAGYKTFDGRGAQVYIYNGPCVFKRVSNI 138

RESULT 2
 MPAL JUNAS STANDARD; PRT; 367 AA.
 AC P81294; O92NU7; Rel. 40; Created
 DT 16-OCT-2001 (Rel. 40; Last sequence update)
 DT 15-JUN-2002 (Rel. 41; Last annotation update)
 DE Major pollen allergen Jun a 1 precursor.
 OS Juniperus ashei (Ozark white cedar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Juniperus.
 OC NCBI_TaxId=13101;
 RN [1]
 RP SEQUENCE FROM N.A., AND SEQUENCE OF 31-38; 42-50; 58-80; 88-94;
 RC TISSUE=Pollen;
 RX MEDLINE=99414163; PubMed=10482836;
 RA Midoro-Horitsu T.M., Goldblum R.M., Kurosky A., Wood T.G.,
 RT "Molecular cloning of mountain cedar (Juniperus ashei) pollen major
 RT allergen, Jun a 1."
 RL J. Allergy Clin. Immunol. 104:613-617(1999).
 RN [2]
 RP SEQUENCE OF 22-50.
 RC TISSUE=Pollen;
 RX MEDLINE=99414162; PubMed=10482835;
 RA Midoro-Horitsu T., Goldblum R.M., Kurosky A., Goetz D.W.,

RA Brooks E.G.;
 RT "Isolation and characterization of the mountain cedar (Juniperus
 RT ashei) pollen major allergen, Jun a 1."
 RL J. Allergy Clin. Immunol. 104:608-612(1999).
 CC -1- DISEASE: THIS PROTEIN CAUSES SEVERAL SEASONAL ALLERGIC RHINITIS
 CC IN NORTH AMERICA.
 CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
 CC AMB A I/AMB A II/CRY J I SUBFAMILY.
 CC
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DR EMBL; AF106663; AAD03609.1; -
 DR EMBL; AF106662; AAD03608.1; -
 DR InterPro; IPR002022; Amb_allergen.
 DR Pfam; PF00544; pec_lyase; 1.
 DR PRINTS; PR00807; AMBALLERGEN.
 KW Allergen; Glycoprotein; Signal.
 FT SIGNAL 1 21
 FT CHAIN 1 21
 FT CARBOHYD 148 148 MAJOR POLLEN ALLERGEN JUN A 1.
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 367 AA; 39824 MW; FC9B81E67562E49 CRC64;

Query Match 21.1%; Score 150; DB 1; Length 367;
 Best Local Similarity 55.8%; Pred. No. 2.4e-08;
 Matches 29; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 73 RPLMTIFSGNMNITKLMKPMYIAGYKTFDGRRAEVSVYHNGAKFRRVDGII 124
 DB 87 KALMTIFSGNMNITKLMKPMYIAGYKTFDGRADVHNGPCPFMRKVSNI 138

RESULT 3
 MPAL CRYJA STANDARD; PRT; 514 AA.
 AC P43212;
 DT 01-NOV-1995 (Rel. 32; Created)
 DT 01-NOV-1995 (Rel. 32; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Possible polysaccharonase precursor (EC 3.2.1.15) (PG) (Pectinase)
 DE (Major pollen allergen Cry j 2) (Cry j II).
 OS Cryptomeria japonica (Japanese cedar).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Cryptomeria.
 OC NCBI_TaxId=3369;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Pollen;
 RX MEDLINE=95010777; PubMed=7926035;
 RA Namba M., Kurose M., Toriogo K., Hino K., Taniguchi Y., Fukuda S.,
 RA Usui M., Kurimoto M.;
 RT "Molecular cloning of the second major allergen, Cry j II, from
 RT Japanese cedar pollen."
 RL FEBS Lett. 353:124-128(1994).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Pollen;
 RX MEDLINE=94271186; PubMed=8002972;
 RA Komiyama N., Sone T., Shimizu K., Morikubo K., Kino K.;
 RT "cDNA cloning and expression of Cry j II the second major allergen of
 RT Japanese cedar pollen."
 RL Biochem. Biophys. Res. Commun. 201:1021-1028(1994).
 RN [3]
 RP SEQUENCE OF 55-64.
 RC TISSUE=Pollen;
 RX MEDLINE=90342988; PubMed=2382797;
 RA Sakaguchi M., Inoue S., Tanai M., Ando S., Usui M., Matsunasi T.,
 RT "Identification of the second major allergen of Japanese cedar


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RT pollen."
RL Allergy 45309-312(1990).
CC -1- CATALYTIC ACTIVITY: Random hydrolysis of 1,4-alpha-D-
CC galactosiduronic linkages in pectate and other galacturonans.
CC -1- SUBCELLULAR LOCATION: SECRETED OR AMYLOPLAST (POTENTIAL).
CC -1- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
CC (POLYGALACTURONASES).
CC -----
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CC -----
DR EMBL: D37765; BAA07021.1; -
DR EMBL: D29772; BAA06172.1; -
DR HSRP: P26509; 1BHE.
DR InterPro: IPR000743; GH28.
DR Pfam: PF00295; Glyco_hydro_28; 1.
DR PROSITE: PS00502; POLYGALACTURONASE; 1.
KW Hydrolyase; Glycosidase; Cell wall; Signal; Zymogen; Fruit ripening;
KW Amyloplast; Glycoprotein; Allergen.
FT SIGNAL 1 22 POTENTIAL.
FT PROPEP 23 45 POTENTIAL.
FT CHAIN 46 433 POSSIBLE POLYGALACTURONASE.
FT ACT_SITE 278 278 POTENTIAL.
FT CARBOHYD 460 460 PROBABLE.
FT CARBOHYD 472 472 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CONFLICT 5 5 F -> L (IN REF. 2).
FT CONFLICT 12 12 V -> L (IN REF. 2).
FT CONFLICT 34 35 D -> V (IN REF. 2).
FT CONFLICT 37 37 Q -> K (IN REF. 2).
FT CONFLICT 88 88 K -> N (IN REF. 2).
FT CONFLICT 98 98 N -> S (IN REF. 2).
FT CONFLICT 451 451 K -> E (IN REF. 2).
FT CONFLICT 454 454 G -> R (IN REF. 2).
FT CONFLICT 504 504 M -> I (IN REF. 2).
FT CONFLICT 507 507 R -> C (IN REF. 2).
SQ SEQUENCE 514 AA; 56645 MW; 624611C3FA8D6302 CRC64;

Query Match 20.9%; Score 148.5; DB 1; Length 514;
Best Local Similarity 41.4%; Pred. No. 4.9e-08;
Matches 41; Conservative 8; Mismatches 21; Indels 29; Gaps 2;

QY 31 IDIPASKNHLCKNTGCRMRKNNRIMQFAKLGTLMGRPLMIFSGNMNKLKMP 90
DB 236 IDIFASKNHLCKNTGCRMRKNNRIMQFAKLGTLMGRPLMIFSGNMNKLKMP 272
QY 91 MYLAGYKTFPDG-----RRAEVYVHVGAKFRRVDGI 123
DB 273 ICGPHGISIGSLGRENSEAEVSYVHVGAKFRRVDGI 311

RESULT 4
MPAL_CUPAR STANDARD; PRT; 346 AA.
AC 09SGG9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Major pollen allergen Cup a 1.
OS Cupressus arizonica.
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Cupressus.
CC NCBI_TaxID=49011;
RN (1)
RP SEQUENCE FROM N.A.
RX MEDLINE=20571526; PubMed=1122214;
RA Acetuno E., Del Pozo V., Minguez A., Arrieta I., Cortegano I.,
RA Cardaba B., Gallardo S., Rojo M., Palomino P., Lahoz C.;

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RT "Molecular cloning of major allergen from Cupressus arizonica pollen:
RT Cup a 1."
RL Clin. Exp. Allergy 30:1750-1758(2000).
CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
CC AMB A II/CRY J I SUBFAMILY.
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CC -----
DR EMBL: AJ243570; CAB62551.1; -
DR InterPro: IPR002022; Amb_allergen.
DR Pfam: PF00544; pec_lyase1.
DR PRINTS: PR00807; AMBALLERGEN.
KW Allergen; Glycoprotein.
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 157 157 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 272 272 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 346 AA; 37589 MW; F1281DDDA1D5DFD0 CRC64;

Query Match 20.1%; Score 143; DB 1; Length 346;
Best Local Similarity 53.8%; Pred. No. 1.2e-07;
Matches 28; Conservative 8; Mismatches 16; Indels 0; Gaps 0;

QY 73 RPLMIFSGNMNKLKMPYVAGYKTFPDGRRAEVYVHVGAKFRRVDGI 124
DB 66 KALMIFSGNMNKLKMPYVAGYKTFPDGRRAEVYVHVGAKFRRVDGI 117

RESULT 5
MPAL_CHAOB STANDARD; PRT; 375 AA.
AC 096385;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Major pollen allergen Cha o 1 precursor.
OS Chamaecyparis obtusa (Japanese cypress).
CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
CC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae;
CC Chamaecyparis.
CC NCBI_TaxID=13415;
RN (1)
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Pollen;
RX MEDLINE=96265194; PubMed=8676896;
RA Suzuki M., Komiyama N., Itoh H., Sone T., Kuno K., Takagi I.,
RA Ohta N.;
RT "Purification, characterization and molecular cloning of Cha o 1, a
RT major allergen of Chamaecyparis obtusa (Japanese cypress) pollen."
RL Mol. Immunol. 33:451-460(1996).
CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
CC AMB A II/CRY J I SUBFAMILY.
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CC -----
DR EMBL: D45404; BAA08246.1; -
DR InterPro: IPR002022; Amb_allergen.
DR Pfam: PF00544; pec_lyase1.
DR PRINTS: PR00807; AMBALLERGEN.
KW Allergen; Glycoprotein; Signal.
FT SIGNAL 1 21 MAJOR POLLEN ALLERGEN CHA O 1.
FT CHAIN 22 375

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FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 148 148 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 293 293 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 352 352 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 375 AA; 40258 MW; 81CD91DF7066DBF CRC64;

Query Match 20.0%; Score 142; DB 1; Length 375;
 Best Local Similarity 57.7%; Pred. No. 1.7e-07;
 Matches 30; Conservative 5; Mismatches 17; Indels 0; Gaps 0;

QY 73 RPLMIIFSGNMNLIKLMPMYIAGYKTPDGRRAEVSYYHNGAKFIRVDGII 124
 DB 87 RSLMIIFSKLNIKLNPLIYAGKTIIDRGAEVHIGNGPGCLFMATVSHVI 138

RESULT 6
 9612 LYCES STANDARD; PRT; 404 AA.

AC P24396;
 DT 01-MAR-1992 (Rel. 21, Created)
 DT 01-MAR-1992 (Rel. 21, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Style development-specific protein 9612 precursor.
 GN 9612.

OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4081;

RA [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. VF36; Tissue=Pisfil;
 RX MEDLINE=9117185; PubMed=2277637;
 RA Bodelier K.A., Smith A.G., Gasser C.S.;
 RT "Regulation of a stylar transmitting tissue-specific gene in
 RT wild-type and transgenic tomato and tobacco."
 RL Mol. Gen. Genet. 224:183-192(1990).

CC -1- FUNCTION: MAY HAVE A ROLE IN THE DEVELOPMENT OF THE TRANSMITTING
 CC TISSUE OF THE STYLE AND/OR IN THE EVENTS RELATED TO POLLINATION
 CC SUCH AS SOME ASPECT IN THE FACILITATION OF COMPATIBLE POLLEN TUBE
 CC GROWTH.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: PREDOMINANTLY FOUND IN THE PISTIL WHERE IT IS

CC FOUND IN THE OUTER FIVE LAYERS OF THE STRANDS OF TRANSMITTING

CC TISSUE WITHIN THE UPPER TWO-THIRDS OF THE STYLE. FOUND AT MUCH

CC LOWER LEVELS IN THE ANTHEIRS AND VEGETATIVE ORGANS.

CC -1- DEVELOPMENTAL STAGE: MAXIMUM LEVELS ARE FOUND DURING ANTHESIS.

CC -1- SIMILARITY: 54% IDENTICAL TO TOMATO PROTEIN P59 (AC P15722)

CC AND P56 (AC P15721).

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CC EMBL; X55193; CAA38979.1; -.

DR PIR; S12209; S12209.

DR InterPro; IPR002022; Amb allergen.

DR Pfam; PF00544; Pec lyase1.1.

DR PRINTS; PRO0607; AMBALERGEN.

KW Signal.

FT SIGNAL 1 20

FT CHAIN 21 404

FT CARBOHYD 37 37

FT CARBOHYD 191 191

SQ SEQUENCE 404 AA; 44298 MW; B26ED59B128D8675 CRC64;

Query Match 14.5%; Score 103; DB 1; Length 404;
 Best Local Similarity 30.8%; Pred. No. 0.0021;

Matches 33; Conservative 13; Mismatches 31; Indels 30; Gaps 4;

QY 28 GRRIDIPASNNFHLQKKTIGTRKNNRNIW-----IOFAKLTFTLM 70
 DB 67 GKSPAFSYCAIGGKNAIG-----GKNGRIYVTTDSGNDPVPKPGTLRHA-----VI 116

QY 71 GRRPLMTIFSGNMNLIKLMPMYIAGYKTPDGRRAEVSYYHNGAKFI 117
 DB 117 QDEPLMTIFKRDVNIQLKQELVNNSYTIDGRAS---VHISGPGCI 160

RESULT 7
 MP11 AMBAR STANDARD; PRT; 396 AA.

AC P27759;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pollen allergen Amb a 1.1 precursor (Antigen E) (Antigen Amb a I).
 OS Ambrosia artemisiifolia (Short ragweed).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
 OC Helianthaceae; Ambrosia.
 OX NCBI_TaxID=4212;

RA [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.

RC TISSUE=Pollen;

RX MEDLINE=91093235; PubMed=1702434;

RA Ratnat T., Griffith J.J., Kuo M.-C., Bond J.F., Rogers B.L.,

RA Klapper D.G.;

RT "Cloning of Amb a I (antigen E), the major allergen family of short

RT ragweed pollen.";

RL J. Biol. Chem. 266:1229-1236(1991).

RN [2]
 RP SEQUENCE FROM N.A., AND VARIANTS.

RC TISSUE=Pollen;

RX MEDLINE=92234570; PubMed=1809687;

RA Griffith J.J., Pollock J., Klapper D.G., Rogers B.L., Nault A.K.;

RT "Sequence polymorphism of Amb a I and Amb a II, the major allergens

RT in Ambrosia artemisiifolia (short ragweed)."

RL Int. Arch. Allergy Appl. Immunol. 96:296-304(1991).

CC -1- SUBUNIT: MONOMER.

CC -1- TISSUE SPECIFICITY: POLLEN AND FLOWERS.

CC -1- PM: The N-terminus is blocked.

CC -1- DISSE: ONE OF THE MAJOR ALLERGENS OF THE RAGWEED POLLEN.

CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LASE FAMILY 1.

CC AMB A I/AMB A II/CRY J I SUBFAMILY.

CC -----
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CC EMBL; M63116; -; NOT ANNOTATED_CDS.

DR EMBL; M80558; AAA32665.1; -.

DR PIR; A39099; A39099.

DR PIR; A53240; A53240.

DR InterPro; IPR002022; Amb allergen.

DR Pfam; PF00544; Pec lyase1.1.

DR PRINTS; PRO0607; AMBALERGEN.

KW Antigen; Allergen; Signal; Multigene family; Polymorphism.

FT SIGNAL 1 25

FT CHAIN 26 396

FT VARIANT 92 92

SQ SEQUENCE 396 AA; 42709 MW; 0CE7DDECB28841D CRC64;

Query Match 13.9%; Score 98.5; DB 1; Length 396;
 Best Local Similarity 34.7%; Pred. No. 0.006;
 Matches 26; Conservative 12; Mismatches 22; Indels 15; Gaps 3;

QY 73 RPLWIFSGNNMNIKLMKMPYIAGYKTFDGRRAEVSIVH-----VNGAK--FIRRDV----- 121
 DB 113 RPLWIFSGNNMNIKLMKMPYIAGYKTFDGRRAEVSIVH-----VNGAK--FIRRDV----- 122
 QY 122 -----GIIAYQNPAS 132
 DB 173 VNPGLIKNSDGPAA 187

RESULT 8
 MP13_AMBAR STANDARD; PRT; 397 AA.

AC P27761;
 DT 01-AUG-1992 (Rel. 23, Created)
 DT 01-AUG-1992 (Rel. 23, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Pollen allergen Amb a 1.3 precursor (Antigen E) (Antigen Amb a I).
 OS Ambrosia, Vitidiplantae, Streptophyta, Embryophyta, Tracheophyta;
 OC Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
 OC Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
 OC Asteridae, euasterids II, Asterales, Asteraceae, Asteroideae;
 OC Helianthaceae, Ambrosia.
 NCBI_TaxID=4212;
 RX MEDLINE=9109335; PubMed=1702434;
 RA Rafnar T., Griffith I.J., Kuo M.-C., Bond J.F., Rogers B.L.,
 RA Klapper D.G.,
 RT "Cloning of Amb a I (antigen E), the major allergen family of short
 RT ragweed pollen."
 RL J. Biol. Chem. 266:1229-1236(1991).
 RP SEQUENCE FROM N.A., AND VARIANTS.

RC TISSUE=Pollen;
 RX MEDLINE=92234570; PubMed=1809687;
 RA Griffith I.J., Pollock J., Klapper D.G., Rogers B.L., Nault A.K.,
 RT "Sequence polymorphism of Amb a I and Amb a II, the major allergens
 RT in Ambrosia attenuifolia (short ragweed)."
 RL Int. Arch. Allergy Appl. Immunol. 96:296-304(1991).
 CC -1- SUBUNIT: MONOMER.
 CC -1- TISSUE SPECIFICITY: POLLEN AND FLOWERS.
 CC -1- PTM: The N-terminus is blocked.
 CC -1- DISEASE: ONE OF THE MAJOR ALLERGENS OF THE RAGWEED POLLEN.
 CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
 CC AMB A I/AMB A II/CRY J I SUBFAMILY.

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 CC -----
 CC EMBL, M62961; AAA32668.1; -;
 CC EMBL, M80560; AAA32669.1; ALT_SEQ.
 CC PIR, C39099; C39099.
 CC InterPro, IPR002022; Amb_allergen.
 CC Pfam, PF00544; pec_lyase; 1.
 CC PRINTS; PR00807; AMBALLERGEN.
 CC Antigen; Allergen; signal; Multigene family; Polymorphism.
 CC SIGNAL 1 25
 CC CHAIN 26 397
 CC VARIANT 48 48
 CC SEQUENCE 397 AA; 42928 MW; C8DB41257590DD0A CRC64;

Query Match 13.6%; Score 97; DB 1; Length 397;
 Best Local Similarity 29.5%; Pred. No. 0.0086;
 Matches 31; Conservative 7; Mismatches 33; Indels 34; Gaps 3;

QY 52 WKNRRIWLO-----PAKLT-----GFTLMGRPLWITIF 79

DB 61 WNNRQALADCAOGFAKGYTGKMGDVYTVTSNLDVDPANPKETLRFAAONRPLWITIF 120
 QY 80 SGNNMNIKLMKMPYIAGYKTFDGRRAEVSIVH-----VNGAK--FIRRDV----- 124
 DB 121 KNDVWVNLNGLVNSDKTIDGKGVKEI--INGGLTIANVKNI 163

RESULT 9
 PEL_TOBAC STANDARD; PRT; 397 AA.

AC P40972;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 15-DEC-1998 (Rel. 37, Last annotation update)
 DE Pectate lyase precursor (EC 4.2.2.2).
 OS Nicotiana glauca (Common tobacco).
 OC Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta;
 OC Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots;
 OC Asteridae, euasterids I, Solanales, Solanaceae, Nicotiana.
 NCBI_TaxID=4097;
 RX MEDLINE=93043039; PubMed=1421152;
 RA Rogers H.J., Harvey A., Lonsdale D.M.,
 RT "Isolation and characterization of a tobacco gene with homology to
 RT pectate lyase which is specifically expressed during
 RT microsporogenesis."
 RL Plant Mol. Biol. 20:493-502(1992).
 CC -1- CATALYTIC ACTIVITY: Elimnative cleavage of pectate to give
 CC oligosaccharides with 4-deoxy-alpha-D-gluc-4-enuronosyl groups at
 CC their non-reducing ends.
 CC -1- DEVELOPMENTAL STAGE: MAXIMALLY EXPRESSED LATE IN POLLEN
 CC DEVELOPMENT.

CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
 CC -----
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 CC -----
 CC EMBL, X67158; CAA47630.1; -;
 CC EMBL, X67159; CAA47631.1; -;
 CC EMBL, X67102; CAA43414.1; -;
 CC PIR, S26211; S26211.
 CC InterPro, IPR002022; Amb_allergen.
 CC Pfam, PF00544; pec_lyase; 1.
 CC PRINTS; PR00807; AMBALLERGEN.
 CC KMW lyase; signal.
 CC SIGNAL 1 25
 CC CHAIN 26 397
 CC ACT SITE 272 272
 CC CARBOHYD 134 134
 CC CONFLICT 227 227
 CC CONFLICT 156 156
 CC CONFLICT 189 189
 CC CONFLICT 200 200
 CC CONFLICT 202 202
 CC CONFLICT 249 249
 CC SEQUENCE 397 AA; 44351 MW; EFOA82CE5DA7643F CRC64;

Query Match 13.1%; Score 93; DB 1; Length 397;
 Best Local Similarity 42.9%; Pred. No. 0.022;
 Matches 21; Conservative 7; Mismatches 17; Indels 4; Gaps 2;
 DB 105 YGVIQKBPWITIFGKNNKIKLSRELIVTSNKTIIDGKGFN---VHIONGA 150

RESULT 10

MP12_AMBAR STANDARD; PRT; 398 AA.

AC P27760;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pollen allergen Amb a 1.2 precursor (Antigen K) (Antigen Amb a II).
OS Ambrosia artemisiifolia (short ragweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eustereids II; Asterales; Asteraceae; Asteroideae;
OC Helianthaceae; Ambrosia.
OX NCBI_TaxID=4212;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Pollen;
RX MEDLINE=91093235; PubMed=1702434;
RA Rafnar T., Griffith I.J., Kuo M.-C., Bond J.F., Rogers B.L.,
RA Klapper D.G.;
RT "Cloning of Amb a I (antigen E), the major allergen family of short
ragweed pollen.";
RL J. Biol. Chem. 266:1229-1236(1991).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS.
RC TISSUE=Pollen;
RX MEDLINE=92234570; PubMed=1809687;
RA Griffith I.J., Pollock J., Klapper D.G., Rogers B.L., Nault A.K.;
RT "Sequence polymorphism of Amb a I and Amb a II, the major allergens
in Ambrosia artemisiifolia (short ragweed)."
RL Int. Arch. Allergy Appl. Immunol. 96:296-304(1991).
CC -1- SUBUNIT: MONOMER.
CC -1- TISSUE SPECIFICITY: POLLEN AND FLOWERS.
CC -1- PTM: The N-terminus is blocked.
CC -1- DISEASE: ONE OF THE MAJOR ALLERGENS OF THE RAGWEED POLLEN.
CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
CC AMB A I/AMB A II/CRY J I SUBFAMILY.
CC -----
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CC -----
DR EMBL; M62981; AAA3266.1; -;
DR EMBL; M80559; AAA3266.1; -;
DR PIR; B39099; B39099.
DR InterPro; IPR002022; Amb allergen.
DR Pfam; PF00544; pec_lyase.1.
DR PRINTS; PR00807; AMBALLERGEN.
KW Antigen; Allergen; Signal; Multigene family; Polymorphism.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 398 POLLEN ALLERGEN AMB A 1.2.
FT VARIANT 345 345 R -> K.
FT VARIANT 381 381 L -> I.
SQ SEQUENCE 398 AA; 43664 MW; 020DC662D957416C CRC64;

Query Match 13.1%; Score 93; DB 1; Length 398;
Best Local Similarity 30.5%; Pred. No. 0.022;
Matches 32; Conservative 5; Mismatches 34; Indels 34; Gaps 3;

OY 52 WKNNRIWLO-----FAKLT-----GFTMGRRPMTITF 79
DB 62 WANNRQALADCAQAFAGKTGGRKGDVYTVTSKDDVDVANPKRGTLRFAAQRPLMTITF 121
OY 80 SGNNNITLKMPMYIAGKTGGRRAEVSYVHVGAKFIRRVDTII 124
DB 122 KRNWVHLNOLVNSDKITDGRGVNIT--VAGGLTMNVKNII 164

RESULT 11

MPA2_AMBAR STANDARD; PRT; 397 AA.

AC P27762;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pollen allergen Amb a 2 precursor (Antigen K) (Antigen Amb a II).
OS Ambrosia artemisiifolia (short ragweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; eustereids II; Asterales; Asteraceae; Asteroideae;
OC Helianthaceae; Ambrosia.
OX NCBI_TaxID=4212;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Flower;
RX MEDLINE=92013060; PubMed=1717566;
RA Rogers B.L., Morgenstern J.P., Griffith I.J., Yu X.-B.,
RA Counsel C.M., Brauer A.W., King T.P., Garman R.D., Kuo M.-C.;
RT "Complete sequence of the allergen Amb alpha II. Recombinant
expression and reactivity with T cells from ragweed allergic
patients.";
RL J. Immunol. 147:2547-2552(1991).
RN [2]
RP SEQUENCE FROM N.A., AND VARIANTS.
RC TISSUE=Pollen;
RX MEDLINE=92234570; PubMed=1809687;
RA Griffith I.J., Pollock J., Klapper D.G., Rogers B.L., Nault A.K.;
RT "Sequence polymorphism of Amb a I and Amb a II, the major allergens
in Ambrosia artemisiifolia (short ragweed)."
RL Int. Arch. Allergy Appl. Immunol. 96:296-304(1991).
CC -1- SUBUNIT: MONOMER.
CC -1- TISSUE SPECIFICITY: POLLEN AND FLOWERS.
CC -1- PTM: The N-terminus is blocked.
CC -1- DISEASE: ONE OF THE MAJOR ALLERGENS OF THE RAGWEED POLLEN.
CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
CC AMB A I/AMB A II/CRY J I SUBFAMILY.
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CC -----
DR EMBL; M80561; AAA3267.1; -;
DR PIR; A46469; A46469.
DR InterPro; IPR002022; Amb allergen.
DR Pfam; PF00544; pec_lyase.1.
DR PRINTS; PR00807; AMBALLERGEN.
KW Antigen; Allergen; Signal; Polymorphism.
FT SIGNAL 1 25 POTENTIAL.
FT CHAIN 26 397 POLLEN ALLERGEN AMB A 2.
FT VARIANT 70 70 N -> D (DETECTED ONLY IN FLOWER DNA).
FT VARIANT 138 138 K -> T (DETECTED ONLY IN FLOWER DNA).
FT VARIANT 321 321 K -> R (DETECTED ONLY IN FLOWER DNA).
SQ SEQUENCE 397 AA; 44082 MW; C7861784C9A3D1DD CRC64;

Query Match 12.9%; Score 92; DB 1; Length 397;
Best Local Similarity 42.3%; Pred. No. 0.028;
Matches 22; Conservative 7; Mismatches 21; Indels 2; Gaps 1;

OY 73 RPLMTISGNNNITLKMPMYIAGKTGGRRAEVSYVHVGAKFIRRVDTII 124
DB 114 RPLMTIFORDMTIYLOEMVTVTSKDDVDVANPKRGTLRFAAQRPLMTITF 163
RESULT 12
PE56_LYCSES STANDARD; PRT; 398 AA.
ID PE56_LYCSES
AC P15721;

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GN 01-APR-1990 (Rel. 14, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE Probable pectate lyase P56 precursor (EC 4.2.2.2).
GN LARS6.
OC Lycopersicon esculentum ('Tomato').
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
OX NCBI_TaxId=4081;

[1]
RN SEQUENCE FROM N.A.
RP STRAIN=cv. VF36; TISSUE=Anther;
RC MEDLINE=9132248; PubMed=1983191;
RX Wing R.A., Yamauchi Y., Larabell S.K., Ursin V.M., McCormick S.;
RA "Molecular and genetic characterization of two pollen-expressed genes
RT that have sequence similarity to pectate lyases of the plant pathogen
RL Erwinia."
RN Plant Mol. Biol. 14:17-28(1990).

[2]
RN REVISIONS.
RP STRAIN=cv. VF36; TISSUE=Anther;
RC Wing R.A.; (SEP-1994) to the EMBL/GenBank/DBJ databases.
RL Submitted (SEP-1994) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: MIGHT BE NEEDED DURING POLLEN DEVELOPMENT AND TUBE
CC GROWTH.
CC -1- CATALYTIC ACTIVITY: Eliminative cleavage of pectate to give
CC oligosaccharides with 4-deoxy-alpha-D-gluc-4-enuronosyl groups at
CC their non-reducing ends.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ANTHERS AND POLLEN.
CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.

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CC -----
DR EMBL, X15500; CAA33524.1; -.
DR PIR, S08383; S08383.
DR InterPro, IPR002022; Amb_allergen.
DR Pfam, PF00544; pec_lyase_1.
DR PRINTS, PR00807; AMBALALRGEN.
KW Lyase; Multigene family; Signal.
FT SIGNAL 1 27
FT CHAIN 28 398
FT ACT SITE 273
FT CARBOHYD 135 135
FT CARBOHYD 228 228
FT CARBOHYD N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 398 AA; 44563 MW; 8D676250DB8B8C7C8 CR664;

Query Match 12.8%; Score 91; DB 1; Length 398;
Best Local Similarity 40.8%; Pred. No. 0.036;
Matches 20; Conservative 10; Mismatches 15; Indels 4; Gaps 2.

QY 67 FTLMGRRLPMTITSGNNNTKLMKMPMTIAGYKTPDGRARVSYHV-NGA 114
DB 106 FGVIQKGFMTWTFARSMRIRLTRELIVSSNMKTIDRG--KYVHANGA 151

RESULT 13
ID MP14_AMBAR STANDARD; PRT; 392 AA.
AC P28744;
DT 01-DEC-1992 (Rel. 24, Created)
DT 01-DEC-1992 (Rel. 24, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Pollen allergen Amb a 1.4 precursor (Antigen E) (Antigen Amb a 1).
OS Ambrosia artemisiifolia (Short ragweed).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

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CC Asteridae; eunasteridae II; Asterales; Asteraceae; Asteroideae;
CC Heliantheae; Ambrosia.
OX NCBI_TaxID=4212;
RN [1]
RP SEQUENCE FROM N.A., AND VARIANTS.
RP TISSUE=Pollen;
RX MEDLINE=92234570; PubMed=1809687;
RA Griffith I.J., Pollock J., Klapper D.G., Rogers B.L., Nault A.K.;
RT "sequence polymorphism of Amb a I and Amb a II, the major allergens
  in Ambrosia artemisiifolia (short ragweed)."
  In: Arch. Allergy Appl. Immunol. 96:296-304(1991).
CC -1- SUBUNIT: MONOMER.
CC -1- TISSUE SPECIFICITY: POLLEN AND FLOWERS.
CC -1- PM: The N-terminus is blocked.
CC -1- DISEASE: ONE OF THE MAJOR ALLERGENS OF THE RAGWEED POLLEN.
CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
CC AMB A I/AMB A II/CRY J I SUBFAMILY.
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CC -----
CC DR EMBL; M80562; AAA3670.1; -.
CC DR PIR; D53240;
CC DR InterPro; IPR002022; Amb allergen.
CC Pfam; PF00544; Dec. lyase; 1.
CC PRINTS; PR00807; AMBALLERGEN.
CC DR Antigen; Allergen; Signal; Multigene family; Polymorphism.
CC KW SIGNAL 1 25 POTENTIAL.
CC FT CHAIN 16 392 POLLEN ALLERGEN AMB A 1.4.
CC FT VARIANT 182 188 SHGPPV -> CNDGPPA.
CC SQ SEQUENCE 392 AA; 42842 MW; 7B6219C12F365DA9 CRC64;
CC -----
Query Match 12.5%; Score 89; DB 1; Length 392;
Best Local Similarity 44.2%; Pred. NO. 0.058;
Matches 23; Conservative 7; Mismatches 20; Indels 2; Gaps 1;
OY 73 RPLMTIFSGNNMNLKMPMYIAGYTFDGRAEYSVYVHGAKFRIRVDGII 124
Db 114 RPLMTIFADWYIRDLRELAINNDKTDIGRAKYEIINAGPA--IYVVKII 163
| | | | | : | : | | | | | | | : | : | | | |
| | | | | : | : | | | | | | | : | : | | | |
RESULT 14
PEL_LILLO
ID ID_PEL_LILLO STANDARD; PRT; 434 AA.
AC P40573;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Pecate lyase precursor (EC 4.2.2.2).
DE Lilium longiflorum (Trumpet Lily).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Liliales; Liliaceae;
OC Lilium.
OX NCBI_TaxID=4690;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nellie white; TISSUE=Pollen;
RA Kim S.R., Finkel D.J., An G.;
RL Submitted (JUN-1993) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: Eliminative cleavage of pectate to give
CC oligosaccharides with 4-deoxy-alpha-D-gluc-4-enuronosyl groups at
CC their non-reducing ends.
CC -1- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.
CC -----
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CC -----  
DR EMBL; Z17328; CAA78976.1; -;  
DR EMBL; L18911; AAA33398.1; -;  
DR PIR; S29612; S29612.  
DR InterPro; IP0002022; Amb.allergen.  
DR Pfam; PF00544; Pec.lyase_1.  
DR PRINTS; PR00807; AMBALLERGEN.  
KW Lyase; Signal.  
FT SIGNAL 1 22 POTENTIAL.  
FT CHAIN 23 434 PEPTATE LYASE.  
FT ACT SITE 312 312 POTENTIAL.  
FT CARBOHYD 68 68 N-LINKED (GLCNAC... ) (POTENTIAL).  
FT CARBOHYD 97 97 N-LINKED (GLCNAC... ) (POTENTIAL).  
SQ SEQUENCE 434 AA; 48457 MW; 31FEE30AD2BD064 CRC64;  
  
Query Match 12.5%; Score 89; DB 1; Length 434;  
Best Local Similarity 55.9%; Pred. No. 0.064;  
Matches 19; Conservative 3; Mismatches 12; Indels 0; Gaps 0;  
  
Qy 73 RLPLWIFSGNMNKLKMPMTIAGYKTFDDGRREV 106  
Db 151 RLPLWIFGKSMVIRLKQELINNDKITIDRGANV 184  
|||||..::|||.:.|||  
  
RESULT 15  
PE59_LYCES STANDARD; PRT; 449 AA.  
AC PE59_LYCES STAN572;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 15-JUL-1999 (Rel. 38, Last annotation update)  
DE Probable pectate lyase P59 precursor (EC 4.2.2.2).  
GN LAT59.  
OS Lycopersicon esculentum (Tomato).  
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;  
OX Asteridae; euasterids I; Solanales; Solanaceae; Solanum.  
OX NCBI_TaxId=4081;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=cv. VF36; TISSUE=Anther;  
RX MEDLINE=91322485; PubMed=1983191;  
RA Wing R.A., Yamaguchi J., Larabell S.K., Ursin V.M., McCormick S.;  
RT "Molecular and genetic characterization of two pollen-expressed genes  
RT that have sequence similarity to pectate lyases of the plant pathogen  
RT Erwinia";  
RL Plant Mol. Biol. 14:17-28(1990).  
CC -!- FUNCTION: MIGHT BE NEEDED DURING POLLEN DEVELOPMENT AND TUBE  
CC GROWTH.  
CC -!- CATALYTIC ACTIVITY: Eliminative cleavage of pectate to give  
CC oligosaccharides with 4-deoxy-alpha-D-gluc-4-enuronosyl groups at  
CC their non-reducing ends.  
CC -!- TISSUE SPECIFICITY: EXPRESSED IN ANTHERS AND POLLEN  
CC -!- SIMILARITY: BELONGS TO THE POLYSACCHARIDE LYASE FAMILY 1.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -  
CC the European Bioinformatics Institute. There are no restrictions on its  
CC use by non-profit institutions as long as its content is in no way  
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/  
CC or send an email to license@isb-sib.ch).  
CC -----  
DR EMBL; X15499; CAA33523.1; -;  
DR PIR; S27098; S27098.  
DR InterPro; IP0002022; Amb.allergen.  
DR Pfam; PF00544; pec.lyase_1.  
DR PRINTS; PR00807; AMBALLERGEN.  
KW Lyase; Multigene family; Signal.  
FT SIGNAL 1 22 POTENTIAL.
```

FT	CHAIN	23	449	POTABLE PEPTIDE LYASE P59.
FT	ACT SITE	325	325	POTENTIAL.
FT	CARBOHYD	36	56	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	80	80	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	81	81	N-LINKED (GLCNAC. . .) (POTENTIAL).
SO	SEQUENCE	449 AA;	50893 MW;	17E3AM13P173B03C CRC64;

Query Match

Best Local Similarity	11.6%;	Score 82.5;	DB 1;	Length 449;
Matches 39;	Conservative 13;	Mismatches 48;	Indels 75;	Gaps 7;

Qy	3	VTVAFNPGFNRREVFIFKRSVNIHGRRIDIFASNNFHLQNTIGTGR	51
Db	57	VTLAFNQ---KLKDKIMKELKKY-----KGIHNNSTRGLSTKKTGTCPCWYNP	101
Qy	52	-----WKNRRIWLOFAKLTGFTLMG-----	71
Db	102	IDRCMKCDPMWADNRRKKLADCAMGSGKAIQKDGEEFYVTJDNSDVYNDKPGTLRHAVI	161
Qy	72	-RRRLTIFSGMNNIKLKMPYLIACYTFEDRRRLVSVYHY-NGA-----KFTIRRV	120
Db	162	QKRPWLIIIRKGGNNIRLHOEMIMOSDKTIDRRGVN---VHITKGAGITLQYINNV	213

Search completed: May 5, 2003, 16:57:32
Job time : 21 secs

GenCore version 5.1.4.p5.4578
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:54:26 ; Search time 84 Seconds
(without alignments)
328.694 Million cell updates/sec

Title: US-09-142-524D-3
Perfect score: 711
Sequence: 1 MKVTAFNFGFNRRVFIKR.....KFIKRVGIIAAYQNPASWK 134

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits, satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_21.*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	188	26.4	374	10	Q8RUR1 O8RUR1 cryptomeria
2	150	21.1	367	10	Q91LT2 juniperus v
3	150	21.1	367	10	Q91LTI juniperus v
4	150	21.1	367	10	Q9W4S6 O9W4S6 cupressus s
5	150	21.1	367	10	Q9W4S4 O9W4S4 cupressus s
6	150	21.1	367	10	Q9W4S3 O9W4S3 cupressus s
7	150	21.1	367	10	Q9W4S2 O9W4S2 cupressus s
8	150	21.1	367	10	Q9W4S1 O9W4S1 juniperus o
9	146	20.5	367	10	Q9W4S5 O9W4S5 cupressus s
10	144	20.3	367	10	Q9W4S6 O9W4S6 cupressus a
11	110.5	15.5	501	10	Q93X04 O93X04 arabisidopsis
12	110.5	15.5	542	10	Q9SV40 O9SV40 arabisidopsis
13	107.5	15.1	507	10	Q9FY19 O9FY19 juniperus a
14	104.5	14.7	463	10	Q9SCP2 O9SCP2 arabisidopsis
15	100.5	14.1	453	10	Q94LR5 O94LR5 oryza sativ
16	99	13.9	472	10	Q9LFP5 Q9LFP5 arabidopsis

17	97	13.6	455	10	Q64510 O64510 arabidopsis
18	95.5	13.4	181	10	Q23666 Q23666 arabidopsis
19	95.5	13.4	410	10	Q9FMK5 Q9FMK5 arabidopsis
20	95.5	13.4	432	10	Q93225 Q93225 arabidopsis
21	95.5	13.4	459	10	Q23665 Q23665 arabidopsis
22	95.5	13.4	459	10	Q9M982 Q9M982 arabidopsis
23	95	13.4	392	10	Q9FM66 Q9FM66 arabidopsis
24	95	13.4	452	10	Q9LRV5 Q9LRV5 arabidopsis
25	94.5	13.3	226	10	Q23667 Q23667 arabidopsis
26	94.5	13.3	354	10	Q940Q1 Q940Q1 arabidopsis
27	94.5	13.3	398	10	Q9M505 Q9M505 vitis vinif
28	94.5	13.3	404	10	Q9SB71 Q9SB71 arabidopsis
29	94.5	13.3	408	10	Q9CSW8 Q9CSW8 arabidopsis
30	94.5	13.3	431	10	Q9F017 Q9F017 arabidopsis
31	93.5	13.2	392	10	Q9FXD8 Q9FXD8 arabidopsis
32	93.5	13.2	407	10	Q9SDW4 Q9SDW4 musa acumin
33	93.5	13.2	408	10	Q9W116 Q9W116 arabidopsis
34	93	13.1	450	10	Q40319 Q40319 medicago sa
35	91.5	12.9	368	10	Q9C8G4 Q9C8G4 arabidopsis
36	90.5	12.7	409	10	Q93XU1 Q93XU1 salix gligi
37	90	12.7	409	10	Q9LTZ0 Q9LTZ0 arabidopsis
38	89.5	12.6	324	10	Q9S345 Q9S345 capsicum an
39	89.5	12.6	398	10	Q43783 Q43783 musa acumin
40	88.5	12.4	297	10	Q9FY87 Q9FY87 arabidopsis
41	88	12.4	438	10	Q43862 Q43862 zea mays (m
42	87	12.2	368	10	Q94FT5 Q94FT5 fragaria an
43	85.5	12.0	416	10	Q9M8Z8 Q9M8Z8 arabidopsis
44	85	12.0	227	10	Q23668 Q23668 arabidopsis
45	84.5	11.9	401	10	Q24554 Q24554 zinnia eleg

ALIGNMENTS

RESULT 1

Q8RUR1 PRELIMINARY; PRT; 374 AA.
AC Q8RUR1;
DT 01-JUN-2002 (TEMBLrel. 21, Created)
DT 01-JUN-2002 (TEMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TEMBLrel. 21, Last annotation update)
DE Cry j 1 precursor.
GN CRY J 1.1 OR CRY J 1.2.
OS Cryptomeria japonica (Japanese cedar).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferales; Cupressaceae; Cryptomeria.
OX NCBI_TaxID=3369;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=POLLEN;
RA Futamura N., Shinohara K.;
RT "Isolation and characterization of cDNAs encoding major allergen Cry j
1 from Cryptomeria japonica pollen."
PL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB081309; BAB86286.1; -.
DR EMBL; AB081310; BAB86287.1; -.
KW SIGNAL.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 374 CRY J 1.
SQ SEQUENCE 374 AA; 40720 MW; 90D0085D24F2BD4 CRC64;

Query Match 26.4%; Score 188; DB 10; Length 374;
Best Local Similarity 71.2%; Pred. No. 2.6e-12;
Matches 37; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

Cy 73 RPIWTFSGNNNITKLKMPWYAGYKTFDGRRAEYVYVNGAKFIRVDGII 124
Db 87 RPLWTFSGNNNITKLKMPWYAGYKTFDGRRAEYVYVNGAKFIRVDGII 138

RESULT 2
Q9LTI2 PRELIMINARY; PRT; 367 AA.

AC Q9LIT2; 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Pollen major allergen 1-2.
OS Juniperus virginiana (Eastern red cedar).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Juniperus.
OX NCBI_TaxId=39584;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21315424; PubMed=11422337;
RA Midoro-Horitsu T.M., Goldblum R.M., Brooks E.G.;
RT "Identification of mutations in the genes for the pollen allergens of
RT eastern red cedar (Juniperus virginiana).";
RL Clin. Exp. Allergy 31:771-778(2001).
DR EMBL; AF151427; AAF80164.1; -
DR InterPro; IPR002022; Amb_allergen.
DR Pfam; PF00544; pec_lyase; 1.
DR PRINTS; PR00807; AMBALLERGEN.
SQ SEQUENCE 367 AA; 39768 MW; 0A6AC2P1BAF89586 CRC64;

Query Match 21.1%; Score 150; DB 10; Length 367;
Best Local Similarity 55.8%; Pred. No. 3.7e-08;
Matches 29; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 73 RPLMIIFSGNMNIIKMKPMYIAGYKTFDGRRAEVSYVHVGAKFIRRDGII 124
Db 87 KTLMIIFSGNMNIIKMKPLVYAGHKTIDRGADVHLGNGGCLFMRKVSHTV 138

RESULT 3
Q9LIT1 PRELIMINARY; PRT; 367 AA.
ID Q9LIT1;
AC Q9LIT1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Pollen major allergen 1-1.
OS Juniperus virginiana (Eastern red cedar).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Juniperus.
OX NCBI_TaxId=39584;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=21315424; PubMed=11422337;
RA Midoro-Horitsu T.M., Goldblum R.M., Brooks E.G.;
RT "Identification of mutations in the genes for the pollen allergens of
RT eastern red cedar (Juniperus virginiana).";
RL Clin. Exp. Allergy 31:771-778(2001).
DR EMBL; AF151429; AAF80166.1; -
DR InterPro; IPR002022; Amb_allergen.
DR Pfam; PF00544; pec_lyase; 1.
DR PRINTS; PR00807; AMBALLERGEN.
SQ SEQUENCE 367 AA; 39708 MW; DCBD1981A7484711 CRC64;

Query Match 21.1%; Score 150; DB 10; Length 367;
Best Local Similarity 55.8%; Pred. No. 3.7e-08;
Matches 29; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 73 RPLMIIFSGNMNIIKMKPMYIAGYKTFDGRRAEVSYVHVGAKFIRRDGII 124
Db 87 KTLMIIFSGNMNIIKMKPLVYAGHKTIDRGADVHLGNGGCLFMRKVSHTV 138

RESULT 4
Q9M4S6 PRELIMINARY; PRT; 367 AA.
ID Q9M4S6;
AC Q9M4S6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cup s 1 pollen allergen.

GN CUPSI.
OS Cupressus sempervirens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Cupressus.
OX NCBI_TaxId=13469;
RN [1]
RP SEQUENCE FROM N.A.
RA Monsalve R.I., Villalba M., Rodriguez R.;
RT "Cloning and expression of Cup s 1, the major allergen of the pollen
RT of Cupressus sempervirens.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF257491; AAF72625.1; -
DR InterPro; IPR002022; Amb_allergen.
DR Pfam; PF00544; pec_lyase; 1.
DR PRINTS; PR00807; AMBALLERGEN.
SQ SEQUENCE 367 AA; 39835 MW; B4B9C60108C2C5A3 CRC64;

QY 73 RPLMIIFSGNMNIIKMKPMYIAGYKTFDGRRAEVSYVHVGAKFIRRDGII 124
Db 87 KALMIIFSGNMNIIKMKPLVYAGHKTIDRGADVHLGNGGCLFMRKVSHTV 138

RESULT 5
Q9M4S4 PRELIMINARY; PRT; 367 AA.
ID Q9M4S4;
AC Q9M4S4;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cup s 1 pollen allergen.
GN CUPSI.
OS Cupressus sempervirens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Cupressus.
OX NCBI_TaxId=13469;
RN [1]
RP SEQUENCE FROM N.A.
RA Monsalve R.I., Villalba M., Rodriguez R.;
RT "Cloning and expression of Cup s 1, the major allergen of the pollen
RT of Cupressus sempervirens.";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF257493; AAF72627.1; -
DR InterPro; IPR002022; Amb_allergen.
DR Pfam; PF00544; pec_lyase; 1.
DR PRINTS; PR00807; AMBALLERGEN.
SQ SEQUENCE 367 AA; 39934 MW; 974D301D74E3D6E CRC64;

Query Match 21.1%; Score 150; DB 10; Length 367;
Best Local Similarity 55.8%; Pred. No. 3.7e-08;
Matches 29; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 73 RPLMIIFSGNMNIIKMKPMYIAGYKTFDGRRAEVSYVHVGAKFIRRDGII 124
Db 87 KALMIIFSGNMNIIKMKPLVYAGHKTIDRGADVHLGNGGCLFMRKVSHTV 138

RESULT 6
Q9M4S3 PRELIMINARY; PRT; 367 AA.
ID Q9M4S3;
AC Q9M4S3;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE Cup s 1 pollen allergen.
GN CUPSI.
OS Cupressus sempervirens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Cupressus.
OX NCBI_TaxId=13469;


```

RN [1]
RP SEQUENCE FROM N.A.
RA Monsalve R.I., Villalba M., Rodriguez R.;
RT "Cloning and expression of Cup s 1, the major allergen of the pollen
  of Cupressus sempervirens.";
RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF257494; AAF72628.1; -
DR InterPro: IPR002022; Amb_allergen.
DR Pfam: PF00544; pec_lyase; 1.
DR PRINTS: PRO0807; AMBALLERGEN.
SQ SEQUENCE 367 AA; 39832 MW;  B5DFBF5A61C07A53 CRC64;

Query Match
  21.1%; Score 150; DB 10; Length 367;
Best Local Similarity 55.8%; Pred. No. 3.7e-08;
Matches 29; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 73 RPLWIFSGNNNIKMKMPYIAGYKTFDGRRAEVSYYVHNGAKFIRVDGII 124
DB 87 KALWIFSGNNNIKMKMPYVAGHKITIDRGADVHLGNGGPCLFMRKVSIVI 138

RESULT 7
Q9MAS2 PRELIMINARY; PRT; 367 AA.
ID Q9MAS2;
AC Q9MAS2;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cup s 1 pollen allergen.
GN CUPs1.
OS Cupressus sempervirens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Cupressus.
RX NCB1_TaxID=13469;
RN [1]
RP SEQUENCE FROM N.A.
RA Monsalve R.I., Villalba M., Rodriguez R.;
RT "Cloning and expression of Cup s 1, the major allergen of the pollen
  of Cupressus sempervirens.";
RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF257495; AAF72629.1; -
DR InterPro: IPR002022; Amb_allergen.
DR Pfam: PF00544; pec_lyase; 1.
DR PRINTS: PRO0807; AMBALLERGEN.
SQ SEQUENCE 367 AA; 39819 MW;  AE7E055A61C07A53 CRC64;

Query Match
  21.1%; Score 150; DB 10; Length 367;
Best Local Similarity 55.8%; Pred. No. 3.7e-08;
Matches 29; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 73 RPLWIFSGNNNIKMKMPYIAGYKTFDGRRAEVSYYVHNGAKFIRVDGII 124
DB 87 KALWIFSGNNNIKMKMPYVAGHKITIDRGADVHLGNGGPCLFMRKVSIVI 138

RESULT 8
Q93X51 PRELIMINARY; PRT; 367 AA.
ID Q93X51;
AC Q93X51;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Putative allergen jun o 1.
GN JUN O 1.
OS Juniperus oxycedrus (prickly juniper).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Juniperus.
RX NCB1_TaxID=69008;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=POTLEN;
RC TISSUE=POTLEN;
FT TISSUE=POTLEN;
SQ SEQUENCE 367 AA; 39809 MW;  AEF7260423A9F28 CRC64;
  "Cloning of Juniperus oxycedrus major allergen.";

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RL Submitted (AUG-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AJ293767; CAC48400.1; -
DR InterPro: IPR002022; Amb_allergen.
DR Pfam: PF00544; pec_lyase; 1.
SQ SEQUENCE 367 AA; 39808 MW;  5D28204DBFD1B9D7 CRC64;

Query Match
  21.1%; Score 150; DB 10; Length 367;
Best Local Similarity 55.8%; Pred. No. 3.7e-08;
Matches 29; Conservative 9; Mismatches 14; Indels 0; Gaps 0;

QY 73 RPLWIFSGNNNIKMKMPYIAGYKTFDGRRAEVSYYVHNGAKFIRVDGII 124
DB 87 KALWIFSGNNNIKMKMPYVAGHKITIDRGADVHLGNGGPCLFMRKVSIVI 138

RESULT 9
Q9MAS5 PRELIMINARY; PRT; 367 AA.
ID Q9MAS5;
AC Q9MAS5;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Cup s 1 pollen allergen.
GN CUPs1.
OS Cupressus sempervirens.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Cupressus.
RX NCB1_TaxID=13469;
RN [1]
RP SEQUENCE FROM N.A.
RA Monsalve R.I., Villalba M., Rodriguez R.;
RT "Cloning and expression of Cup s 1, the major allergen of the pollen
  of Cupressus sempervirens.";
RL Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF257492; AAF72626.1; -
DR InterPro: IPR002022; Amb_allergen.
DR Pfam: PF00544; pec_lyase; 1.
DR PRINTS: PRO0807; AMBALLERGEN.
SQ SEQUENCE 367 AA; 39894 MW;  5D56FC0E3263B741 CRC64;

Query Match
  20.5%; Score 146; DB 10; Length 367;
Best Local Similarity 53.8%; Pred. No. 1e-07;
Matches 28; Conservative 10; Mismatches 14; Indels 0; Gaps 0;

QY 73 RPLWIFSGNNNIKMKMPYIAGYKTFDGRRAEVSYYVHNGAKFIRVDGII 124
DB 87 KALWIFSGNNNIKMKMPYVAGHKITIDRGADVHLGNGGPCLFMRKVSIVI 138

RESULT 10
Q93XL6 PRELIMINARY; PRT; 367 AA.
ID Q93XL6;
AC Q93XL6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Putative allergen Cup a 1 precursor.
GN CUP A 1.
OS Cupressus arizonica.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Cupressus.
RX NCB1_TaxID=49011;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=POTLEN;
RC TISSUE=POTLEN;
FT TISSUE=POTLEN;
SQ SEQUENCE 367 AA; 39809 MW;  AEF7260423A9F28 CRC64;
  "Cloning of Cupressus arizonica major allergen.";

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QY 91 MYIAGKTFDGS-----BRAEVSYVHNGAKFIRRVDDGI 123
DB 274 TCGPFGHMSIGSLGKGNRSSEVSFVHLDGAKITDTONGL 312

RESULT 14

Q9SCP2 PRELIMINARY; PRT; 463 AA.

AC Q9SCP2;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE Pectate lyase-like protein.
GN TAD2.120
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosside II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_Taxid=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Nyakatura G., Fartmann B., Dauner D., Sterr W., Holland R.,
RA Weichselgartner M., Mewes H.W., Lemcke K., Mayer K.F.X., Queciet F.,
RA Salanoubat M.;
RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Arabidopsis sequencing project;
RA Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
RL EMBL; AL132958; CAB64222.1; -
DR InterPro; IPR002022; Amb_allergen.
DR Pfam; PF00544; pec_lyase; 1.
DR PRINTS; PR00807; AMBALLERGEN.
KM Lyase.
SQ SEQUENCE 463 AA; 51225 MW; 3424B0DE4ADBA604 CRC64;

Query Match 14.7%; Score 104.5; DB 10; Length 463;
Best Local Similarity 30.5%; Pred. No. 0.0047;
Matches 32; Conservative 8; Mismatches 32; Indels 33; Gaps 3;

QY 52 WKNNRIWL-----QPAKLTG-----FTLMGRPIWITF 79
DB 66 WPNNRQGLADCGIGCGYALGKGGCFYFTDSSDDAVNPKPGLRYGVIGSEPLIVF 125
QY 80 SGNNNITKLKMPWTAGYKTFDGRRAEVSYVHNGAKFIRRVDDGI 124
DB 126 PSNNMILKQELLFNSYKTIIDGRGANVHYIG-GCITLQYVSNII 169

RESULT 15

Q94LR5 PRELIMINARY; PRT; 453 AA.

AC Q94LR5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Putative pectate lyase.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Euphorbiaceae; Oryzae; Oryza.
OX NCBI_Taxid=4530;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CV. NIPPONBARE;
RA Buell C.R., Yuan Q., Ouyang S., Moffat K.S., Hill J.N., Gansberger K.,
RA Brenner M., Burgess S., Hance W., Shvartsbeyn M., Tsilirtin T.,
RA Riggs F., Hsiao J., Zismann V., Blunt S., Pai G., VanAken S.E.,
RA Uteback T.R., Feildblum T.V., Quackenbush J., Salzberg S.L.,
RA White O., Fraser C.M.;
RT "Oryza sativa chromosome 10 BAC OSUNB0011A08 genomic sequence."
RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AC034258; AAK54283.1; -.

DR InterPro; IPR002022; Amb_allergen.
DR Pfam; PF00544; pec_lyase; 1.
KM Lyase.
SQ SEQUENCE 453 AA; 48006 MW; 1411BBE1A40901DC CRC64;

Query Match 14.1%; Score 100.5; DB 10; Length 453;
Best Local Similarity 48.8%; Pred. No. 0.013;
Matches 20; Conservative 7; Mismatches 13; Indels 1; Gaps 1;

QY 74 PLMTIFSGNNITKLKMPWTAGYKTFDGRRAEVSYVHNGA 114
DB 140 PLMTIFAGDWTIRLNEBLVNSYKTIIDGRGANV-HYGAGGA 179

Search completed: May 5, 2003, 16:59:01
Job time: 90 secs

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: May 5, 2003, 16:48:06 ; Search time 46 Seconds
(without alignments)
388.165 Million cell updates/sec

Title: US-09-142-524D-3

Perfect score: 711
Sequence: 1 MKVTAVAPNGPQPRNRVRIK.....KTRIVDGIITAYQNPASWK 134

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 908470 seqs, 133250620 residues

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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2: /SID2/gcgdata/geneseq/geneseq-emb1/AA1981.DAT.*
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22: /SID2/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*
23: /SID2/gcgdata/geneseq/geneseq-emb1/AA2002.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	711	100.0	134	AAW27371	Multi-epitope pep
2	523.5	73.6	105	AAW27370	Multi-epitope pep
3	320	45.0	80	AAW27369	Multi-epitope pep
4	198.5	27.9	214	AAW69120	Cedar pollen aller
5	188	26.4	353	AAW75388	Japanese cedar pol
6	188	26.4	353	AAW81587	Cedar pollen aller
7	188	26.4	373	AAW25664	Cedar pollen aller
8	188	26.4	373	AAW25668	Japanese cedar all
9	188	26.4	374	AAW1937	Cry j I. Cryptome
10	188	26.4	374	AAW45541	Cry j I pollen all

11	188	26.4	374	15	AAW60166	Japanese cedar pol
12	188	26.4	374	16	AAW82490	Cry j I Japanese C
13	188	26.4	374	20	AAW25665	Cedar allergen 493
14	188	26.4	374	20	AAW25669	Japanese cedar all
15	178	25.0	210	22	AAW69103	Cedar pollen aller
16	162	22.8	96	22	AAW69104	Cedar pollen aller
17	162	22.8	96	22	AAW69119	Cedar pollen aller
18	162	22.8	97	22	AAW69105	Cedar pollen aller
19	150	21.1	367	15	AAW45577	Jun s I. Juniperu
20	150	21.1	370	15	AAW45578	Jun v I. Juniperu
21	148.5	20.9	460	16	AAW69791	Japanese cedar aller
22	148.5	20.9	514	15	AAW53690	Japanese cedar pol
23	148.5	20.9	514	16	AAW74333	Japanese cedar pol
24	148.5	20.9	514	16	AAW69792	Japanese cedar pol
25	148.5	20.9	514	17	AAW93599	Japanese cedar pol
26	148.5	20.9	514	17	AAW81586	Japanese cedar all
27	148.5	20.9	514	20	AAW25667	Japanese cedar all
28	148.5	20.9	514	20	AAW25667	Japanese cedar all
29	148	20.8	186	22	AAW69102	Japanese cedar all
30	142	20.0	354	17	AAW04344	Chamaecyparis obtu
31	142	20.0	354	19	AAW42121	Chamaecyparis obtu
32	142	20.0	375	17	AAW04345	Chamaecyparis obtu
33	141.5	19.9	93	22	AAW69117	Cedar pollen aller
34	136	19.1	30	21	AAW44682	Artificial sequenc
35	120.5	16.9	74	21	AAW23905	Artificial sequenc
36	120.5	16.9	94	21	AAW23906	Artificial sequenc
37	120.5	16.9	95	21	AAW23897	Artificial sequenc
38	120.5	16.9	95	21	AAW23901	Artificial sequenc
39	120.5	16.9	95	22	AAW69098	Cedar pollen aller
40	120.5	16.9	99	21	AAW23802	Artificial sequenc
41	120.5	16.9	99	21	AAW23807	Artificial sequenc
42	120.5	16.9	99	22	AAW69099	Cedar pollen aller
43	118.5	16.7	514	17	AAW04346	Chamaecyparis obtu
44	118.5	16.7	514	19	AAW42122	Chamaecyparis obtu
45	117	16.5	47	19	AAW80353	Sugi allergen prot

ALIGNMENTS

RESULT 1
AAW27371
ID AAW27371 standard; peptide; 134 AA.
-XX
AC AAW27371;
XX 24-MAR-1998 (first entry)
DT
XX Multi-epitope peptide used as immunotherapeutic agent #3.
DE
XX Multi-epitope peptide; immunotherapeutic agent; allergic disease;
KW T-cell epitope region; allergen; lymphocyte; immunoglobulin E.
XX
XX Synthetic.
XX
XX WO9732600-A1.
XX
XX 12-SEP-1997.
XX
XX 10-MAR-1997; 97WO-JP00740.
XX
XX 10-MAR-1996; 96JP-0080702.
XX
XX (MEIP) MEIJI MILK PROD CO LTD.
XX
XX Dai-ichi K, Iwama A, Kino K, Kume A, Some T;
XX WPI, 1997-470495/43.
XX
XX Peptide immuno:therapeutic agent to treat allergic diseases -
XX contains multi-epitope peptide containing T cell epitope regions
XX from different allergens

PS Claim 6; Page 32; 58pp; Japanese.
XX
CC The present sequence represents a multi-epitope peptide which is used as
CC a new immunotherapeutic agent. It comprises T cell epitope regions from 2
CC or more different allergens (preferably linked via arginine or lysine
CC dimers), where the T cell epitope regions have a positivity index
CC greater than 100 as measured in a patient group responding to the
CC allergen; have at least 70% reactivity with lymphocytes from patients
CC responding to the allergen; and are not reactive with immunoglobulin E
CC (IgE) antibodies from patients responsive to the allergen. The agent can
CC be used to prevent and treat a wide variety of allergic diseases, e.g. by
CC desensitisation. Side effects, e.g. those mediated by IgE, are reduced.
XX
SQ Sequence 134 AA;
Query Match 100.0%; Score 711; DB 18; Length 134;
Best Local Similarity 100.0%; Pred. No. 1.7e-82;
Matches 134; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKYTVAFNPGPVRVFIKRVSVIIHGRIDIFASKNHLQNTIGTRRMKNRIWQ 60
DB 1 MKYTVAFNPGPVRVFIKRVSVIIHGRIDIFASKNHLQNTIGTRRMKNRIWQ 60
QY 61 FAKLTGFTLMGRPLMIFSGNMNIIKMKPMYIAGYKTFDGRRAVSYVHVGAKFIRRV 120
DB 61 FAKLTGFTLMGRPLMIFSGNMNIIKMKPMYIAGYKTFDGRRAVSYVHVGAKFIRRV 120
QY 121 DGIIAAYONPASWK 134
DB 121 DGIIAAYONPASWK 134
RESULT 2
AAW27370
ID AAW27370 standard; peptide; 105 AA.
AC AAW27370;
XX
XX 24-MAR-1998 (first entry)
DT
DE Multi-epitope peptide used as immunotherapeutic agent #2.
XX
XX Multi-epitope peptide; immunotherapeutic agent; allergic disease;
KW T-cell epitope region; allergen; lymphocyte; immunoglobulin E.
XX
XX Synthetic.
OS
XX WO9732600-A1.
PN
XX
XX 12-SEP-1997.
PD
XX 10-MAR-1997; 97WO-JP00740.
PF
XX 10-MAR-1996; 96JP-0080702.
PR
XX 10-MAR-1996; 96JP-0080702.
PA (MEIP) MEIJI MILK PROD CO LTD.
XX
PI Daiichi K, Iwama A, Kino K, Kume A, Sone T;
XX
XX WPI; 1997-470495/43.
DR
XX
XX Peptide immuno:therapeutic agent to treat allergic diseases -
PT contains multi-epitope peptide containing T cell epitope regions
PT from different allergens
XX
XX
PS Claim 6; Page 31; 58pp; Japanese.
XX
XX The present sequence represents a multi-epitope peptide which is used as
CC a new immunotherapeutic agent. It comprises T cell epitope regions from 2
CC or more different allergens (preferably linked via arginine or lysine
CC dimers), where the T cell epitope regions have a positivity index
CC greater than 100 as measured in a patient group responding to the
CC allergen; have at least 70% reactivity with lymphocytes from patients
CC responding to the allergen; and are not reactive with immunoglobulin E
CC (IgE) antibodies from patients responsive to the allergen. The agent can
CC be used to prevent and treat a wide variety of allergic diseases, e.g. by
CC desensitisation. Side effects, e.g. those mediated by IgE, are reduced.
XX
SQ Sequence 80 AA;
Query Match 45.0%; Score 320; DB 18; Length 80;

CC responding to the allergen; and are not reactive with immunoglobulin E
CC (IgE) antibodies from patients responsive to the allergen. The agent can
CC be used to prevent and treat a wide variety of allergic diseases, e.g. by
CC desensitisation. Side effects, e.g. those mediated by IgE, are reduced.
XX
SQ Sequence 105 AA;
Query Match 73.6%; Score 523.5; DB 18; Length 105;
Best Local Similarity 78.4%; Pred. No. 9.8e-59;
Matches 105; Conservative 0; Mismatches 0; Indels 29; Gaps 2;
QY 1 MKYTVAFNPGPVRVFIKRVSVIIHGRIDIFASKNHLQNTIGTRRMKNRIWQ 60
DB 1 MKYTVAFNPGPVRVFIKRVSVIIHGRIDIFASKNHLQNTIGTRRMKNRIWQ 60
QY 61 FAKLTGFTLMGRPLMIFSGNMNIIKMKPMYIAGYKTFDGRRAVSYVHVGAKFIRRV 120
DB 61 FAKLTGFTLMGRPLMIFSGNMNIIKMKPMYIAGYKTFDGRRAVSYVHVGAKFIRRV 120
QY 121 DGIIAAYONPASWK 134
DB 92 DGIIAAYONPASWK 105
RESULT 3
AAW27369
ID AAW27369 standard; peptide; 80 AA.
AC AAW27369;
XX
XX 24-MAR-1998 (first entry)
DT
DE Multi-epitope peptide used as immunotherapeutic agent #1.
XX
XX Multi-epitope peptide; immunotherapeutic agent; allergic disease;
KW T-cell epitope region; allergen; lymphocyte; immunoglobulin E.
XX
XX Synthetic.
OS
XX WO9732600-A1.
PN
XX
XX 12-SEP-1997.
PD
XX 10-MAR-1997; 97WO-JP00740.
PF
XX 10-MAR-1996; 96JP-0080702.
PR
XX 10-MAR-1996; 96JP-0080702.
PA (MEIP) MEIJI MILK PROD CO LTD.
XX
PI Daiichi K, Iwama A, Kino K, Kume A, Sone T;
XX
XX WPI; 1997-470495/43.
DR
XX
XX Peptide immuno:therapeutic agent to treat allergic diseases -
PT contains multi-epitope peptide containing T cell epitope regions
PT from different allergens
XX
XX
PS Claim 6; Page 31; 58pp; Japanese.
XX
XX The present sequence represents a multi-epitope peptide which is used as
CC a new immunotherapeutic agent. It comprises T cell epitope regions from 2
CC or more different allergens (preferably linked via arginine or lysine
CC dimers), where the T cell epitope regions have a positivity index
CC greater than 100 as measured in a patient group responding to the
CC allergen; have at least 70% reactivity with lymphocytes from patients
CC responding to the allergen; and are not reactive with immunoglobulin E
CC (IgE) antibodies from patients responsive to the allergen. The agent can
CC be used to prevent and treat a wide variety of allergic diseases, e.g. by
CC desensitisation. Side effects, e.g. those mediated by IgE, are reduced.
XX
SQ Sequence 80 AA;
Query Match 45.0%; Score 320; DB 18; Length 80;


```

XX AC AAR81587;
XX XX
XX DT 24-MAY-1996 (first entry)
XX DE Cedar pollen allergen B.
XX KW Cedar; pollen; allergen; immunoglobulin E; IgE; T-cell epitope;
XX KW antibody; pollinosis; therapy; immunotherapy.
XX OS Cryptomeria japonica.
XX PN EP700929-A2.
XX PD 13-MAR-1996.
XX PF 08-SEP-1995; 95EP-0306295.
XX PR 14-JUL-1995; 95JP-0200221.
XX PR 10-SEP-1994; 94JP-0242137.
XX PR 14-JUL-1995; 95JP-0200204.
XX PA (HAYB) HAYASHIBARA SEIBUTSU KAGAKU.
XX PI Hino K, Saito S, Taniguchi Y;
XX DR WPI; 1996-140976/15.
XX PT New peptide(s) derived from cedar pollen allergens - activate
XX PT allergen-specific T-cells, but not allergen-specific IgE antibodies,
XX PT used for treating cedar pollinosis
XX PS Claim 5; Page 31-32; 36pp; English.
XX CC Synthetic peptides based on portions of cedar pollen allergens A
XX CC (AAR81586) and B (AAR81587) were tested for their ability to activate
XX CC cedar allergen-specific T-cells, but not allergen-specific IgE
XX CC antibodies. 6 Peptides (AAR81580-R81585) were identified as T-cell
XX CC epitopes. These peptides, plus subsequences (AAR81573-79) essential
XX CC for T-cell recognition, and homologous peptides (AAR81588-96) can
XX CC be used as immunotherapeutic agents to treat or prevent cedar
XX CC pollinosis, avoiding side-effects such as anaphylaxis.
XX SQ Sequence 353 AA;

Query Match 26.4%; Score 188; DB 17; Length 353;
Best Local Similarity 71.2%; Pred. No. 3.2e-15;
Matches 37; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 73 RPLWIIIFSGNNMNIKLMMPYIAGYKTFDGRRAEVSYYVHNGAKFIRYDGI 124
DB 66 RPLWIIIFSGNNMNIKLMMPYIAGYKTFDGRRAEVSYYVHNGAKFIRYDGI 117

RESULT 7
ID AAY25664
AY25664 standard; protein; 373 AA.
XX AC AAY25664;
XX DT 30-SEP-1999 (first entry)
XX DE Cedar allergen 493634 Cry j IB protein fragment.
XX KW Major histocompatibility complex; class II; desensitizing; human;
XX KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;
XX KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
XX KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
XX KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
XX KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity; cedar.
XX OS Cedrus sp.
XX PR

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PN WO9934826-A1.
XX XX
XX PD 15-JUL-1999.
XX PF 11-JAN-1999; 99WO-GB00080.
XX PR 21-SEP-1998; 98GB-0020474.
XX PR 09-JAN-1998; 98GB-0000445.
XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX PI Kay AB, Larche M;
XX DR WPI; 1999-45825/38.
XX PT Desensitizing patients to polypeptide allergens
XX PS Example 6; Page 73; 117pp; English.
XX CC This invention describes a novel method of desensitizing a patient to a
XX CC polypeptide allergen and comprises administering to the patient a peptide
XX CC derived from the allergen where restriction to a MHC Class II molecule
XX CC possessed by the patient can be demonstrated for the peptide and the
XX CC peptide is able to induce a late phase response in an individual who
XX CC possesses the MHC Class II molecule. The methods can be used for
XX CC desensitizing patients to allergens present in e.g. grass, tree and weed
XX CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
XX CC the chironomidae (non-biting midges), spiders and mites, housefly, fruit
XX CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
XX CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
XX CC tenbryo molitor beetle, mammals such as cat, dog, horse, cow, pig,
XX CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
XX CC produce immunological vaccines which may be used to prevent and/or treat
XX CC conditions involving hypersensitivity to allergens. This sequence
XX CC represents a cedar (Cedrus sp.) allergen 493634 Cry j IB.
XX SQ Sequence 373 AA;

Query Match 26.4%; Score 188; DB 20; Length 373;
Best Local Similarity 71.2%; Pred. No. 3.5e-15;
Matches 37; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 73 RPLWIIIFSGNNMNIKLMMPYIAGYKTFDGRRAEVSYYVHNGAKFIRYDGI 124
DB 86 RPLWIIIFSGNNMNIKLMMPYIAGYKTFDGRRAEVSYYVHNGAKFIRYDGI 137

RESULT 8
ID AAY25668
AY25668 standard; protein; 373 AA.
XX AC AAY25668;
XX DT 30-SEP-1999 (first entry)
XX DE Japanese cedar allergen 541803 Cry j I precursor protein fragment.
XX KW Major histocompatibility complex; class II; desensitizing; human;
XX KW allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;
XX KW chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
XX KW screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
XX KW cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
XX KW mice; gerbil; vaccine; treatment; prevention; hypersensitivity; cedar.
XX OS Cedrus sp.
XX PN WO9934826-A1.
XX PD 15-JUL-1999.
XX PF 11-JAN-1999; 99WO-GB00080.
XX PR 21-SEP-1998; 98GB-0020474.
XX PR

```


PR 09-JAN-1998; 98GB-0000445.
XX (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX
XX Kay AB, Larche M,
XX WPI; 1999-458255/38.
XX
XX Desensitizing patients to polypeptide allergens
XX
XX Example 6; Page 75; 117pp; English.
XX
XX This invention describes a novel method of desensitizing a patient to a
XX polypeptide allergen and comprises administering to the patient a peptide
XX derived from the allergen where restriction to a MHC Class II molecule
XX possessed by the patient can be demonstrated for the peptide and the
XX peptide is able to induce a late phase response in an individual who
XX possesses the MHC Class II molecule. The methods can be used for
XX desensitizing patients to allergens present in e.g. grass, tree and weed
XX (including ragweed) pollens, fungi and moulds, foods, stinging insects,
XX the chironomidae (non-biting midges), spiders and mites, housefly, fruit
XX fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
XX non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
XX Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
XX sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
XX produce immunological vaccines which may be used to prevent and/or treat
XX conditions involving hypersensitivity to allergens. This sequence
XX represents a Japanese cedar (Cedrus sp.) allergen 541803 Cry j I
XX precursor.
XX
XX Sequence 373 AA;
SQ
Query Match 26.4%; Score 188; DB 20; Length 373;
Best Local Similarity 71.2%; Pred. No. 3.5e-15;
Matches 37; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 73 RPLMIIFSGNNNITLKMPLYAGYKTFDGRRAEVSYYHVGAKFIRRDGII 124
DB 86 RPLMIIFSGNNNITLKMPLYAGYKTFDGRGAQYIYIGNGSPCVFIRKVSNI 137
RESULT 9
ID AAR31937 standard; Protein; 374 AA.
XX
XX AAR31937;
AC
XX 03-JUN-1993 (first entry)
DT
XX
XX Cry j I.
DE
XX
XX Japanese cedar pollen; allergen; antigen; allergy; B cell; T cell.
XX
XX Cryptomeria japonica.
XX
XX Key Location/Qualifiers
XX FH Peptide 1..21
XX FT /note= "signal peptide"
XX FT Protein 22..374
XX FT /note= "mature Cry j I"
XX
XX WO9301213-A.
XX
XX PD 21-JAN-1993.
XX
XX PF 10-JUL-1992; 92WO-US05661.
XX
XX PR 12-JUL-1991; 91US-0729134.
XX PR 15-JUL-1991; 91US-0730452.
XX
XX (IMMU-) IMMUNOLOGIC PHARM CORP.
XX
XX Bond JF, Griffith IU, Pollock J;
PI

XX
XX WPI; 1993-045434/05.
DR N-PSDB; AAQ35304.
XX
XX PT Nucleic acid sequence encoding Cryptomeria japonica allergen -
XX PT for the diagnosis treatment and prevention of allergic reactions
XX PT to Japanese cedar pollen
XX
XX Claim 11; Page 42; 69pp; English.
XX
XX Fresh pollen and staminate cone samples were collected from a single
XX Cryptomeria japonica (Japanese cedar) tree. RNA was prep'd. and used
XX CC to synthesize cDNA. The cDNA was subjected to successive rounds of
XX PCR to yield a full length Cry j I clone. Cry j I or an antigenic
XX fragment of it may be used for detecting, treating and preventing an
XX allergic response to Japanese cedar pollen allergen. It is capable of
XX modifying both the B and T cell response to Cry j I and T cell response
XX to a Cry j I antigen.
XX
XX Sequence 374 AA;
SQ
Query Match 26.4%; Score 188; DB 14; Length 374;
Best Local Similarity 71.2%; Pred. No. 3.5e-15;
Matches 37; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
QY 73 RPLMIIFSGNNNITLKMPLYAGYKTFDGRRAEVSYYHVGAKFIRRDGII 124
DB 87 RPLMIIFSGNNNITLKMPLYAGYKTFDGRGAQYIYIGNGSPCVFIRKVSNI 138
RESULT 10
ID AAR45541 standard; Protein; 374 AA.
XX
XX AAR45541;
AC
XX 13-JUN-1994 (first entry)
DT
XX
XX Cry j I pollen allergen.
DE
XX
XX Japanese cedar; detection; allergy; treatment; diagnosis;
XX KM T cell epitope; sensitivity.
XX
XX Cryptomeria japonica.
XX
XX Key Location/Qualifiers
XX FH Peptide 1..21
XX FT /note= "signal peptide"
XX FT Peptide 22..374
XX FT /note= "mature peptide"
XX
XX WO9401560-A.
XX
XX PD 20-JAN-1994.
XX
XX PF 15-JAN-1993; 93WO-US00139.
XX
XX PR 01-SEP-1992; 92US-0938990.
XX PR 10-JUL-1992; 92WO-US05661.
XX
XX (IMMU-) IMMUNOLOGIC PHARM CORP.
XX
XX PI Bond JF, Garman RD, Griffith IU, Kuo M, Pollock J;
XX
XX WPI; 1994-035066/04.
XX
XX DR N-PSDB; AAQ55271.
XX
XX Antigen derived from Japanese cedar pollen allergen Cry j I -
XX PT contain at least two T cell epitope(s), used to treat or diagnose
XX PT allergy
XX
XX PS Disclosure; Fig 4; 137pp; English.
XX


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XX OS Cedrus sp.
XX PN WO9934826-A1.
XX PD 15-JUL-1999.
XX PF 11-JAN-1999; 99WO-GB00080.
XX PR 21-SEP-1998; 98GB-0020474.
XX PR 09-JAN-1998; 98GB-0000445.
XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX PI Kay AB, Larche M;
XX DR WPI; 1999-458255/38.
XX PT Desensitizing patients to polypeptide allergens
XX PS Example 6; Page 73; 117pp; English.
XX CC This invention describes a novel method of desensitizing a patient to a
XX CC polypeptide allergen and comprises administering to the patient a peptide
XX CC derived from the allergen where restriction to a MHC Class II molecule
XX CC possessed by the patient can be demonstrated for the peptide and the
XX CC peptide is able to induce a late phase response in an individual who
XX CC possesses the MHC Class II molecule. The methods can be used for
XX CC desensitizing patients to allergens present in e.g. grass, tree and weed
XX CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
XX CC the chironomidae (non-biting midges), spiders and mites, housefly, fruit
XX CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
XX CC non-biting midge larvae, bee moth larvae, mealworm, cockroach, larvae of
XX CC Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
XX CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
XX CC produce immunological vaccines which may be used to prevent and/or treat
XX CC conditions involving hypersensitivity to allergens. This sequence
XX CC represents a cedar (Cedrus sp.) allergen 493632 Cry j I A.
XX SQ Sequence 374 AA;
XX
XX Query Match 26.4%; Score 188; DB 20; Length 374;
XX Best Local Similarity 71.2%; Pred. No. 3.5e-15;
XX Matches 37; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
OY 73 RPLMIIFSGNNIKLKMPMYIAGYKTFDGRRAEVSYYHVGAKFIRVDGII 124
DB 87 RPLMIIFSGNNIKLKMPMYIAGYKTFDGRGAQYIYINGSPCVFIRKVSNI 138
RESULT 14
AAV25669
ID AAV25669 standard; protein; 374 AA.
XX AC
XX AAV25669;
XX DT 30-SEP-1999 (first entry)
XX DE Japanese cedar allergen 541802 Cry j I precursor protein fragment.
XX KM Major histocompatibility complex; class II; desensitizing; human;
XX KM allergen; grass; tree; weed; pollen; fungi; mould; food; insect; sting;
XX KM chironomidae; spider; mite; housefly; fruit fly; sheep blow fly; honeybee;
XX KM screw worm fly; grain weevil; silkworm; bee moth; larvae; mealworm; cat;
XX KM cockroach; beetle; dog; horse; cow; pig; sheep; rabbit; rat; guinea pig;
XX KM mice; gerbil; vaccine; treatment; prevention; hypersensitivity; cedar.
XX OS
XX Cedrus sp.
XX PN WO9934826-A1.
XX PD 15-JUL-1999.

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PF 11-JAN-1999; 99WO-GB00080.
XX 21-SEP-1998; 98GB-0020474.
XX PR 09-JAN-1998; 98GB-0000445.
XX PA (IMCO-) IMPERIAL COLLEGE INNOVATIONS LTD.
XX PI Kay AB, Larche M;
XX DR WPI; 1999-458255/38.
XX PT Desensitizing patients to polypeptide allergens
XX PS Example 6; Page 75; 117pp; English.
XX CC This invention describes a novel method of desensitizing a patient to a
XX CC polypeptide allergen and comprises administering to the patient a peptide
XX CC derived from the allergen where restriction to a MHC Class II molecule
XX CC possessed by the patient can be demonstrated for the peptide and the
XX CC peptide is able to induce a late phase response in an individual who
XX CC possesses the MHC Class II molecule. The methods can be used for
XX CC desensitizing patients to allergens present in e.g. grass, tree and weed
XX CC (including ragweed) pollens, fungi and moulds, foods, stinging insects,
XX CC the chironomidae (non-biting midges), spiders and mites, housefly, fruit
XX CC fly, sheep blow fly, screw worm fly, grain weevil, silkworm, honeybee,
XX CC Tenbrio molitor beetle, mammals such as cat, dog, horse, cow, pig,
XX CC sheep, rabbit, rat, guinea pig, mice or gerbil. They can also be used to
XX CC produce immunological vaccines which may be used to prevent and/or treat
XX CC conditions involving hypersensitivity to allergens. This sequence
XX CC represents a Japanese cedar (Cedrus sp.) allergen 541802 Cry j I
XX SQ Sequence 374 AA;
XX
XX Query Match 26.4%; Score 188; DB 20; Length 374;
XX Best Local Similarity 71.2%; Pred. No. 3.5e-15;
XX Matches 37; Conservative 4; Mismatches 11; Indels 0; Gaps 0;
OY 73 RPLMIIFSGNNIKLKMPMYIAGYKTFDGRRAEVSYYHVGAKFIRVDGII 124
DB 87 RPLMIIFSGNNIKLKMPMYIAGYKTFDGRGAQYIYINGSPCVFIRKVSNI 138
RESULT 15
AAB69103
ID AAB69103 standard; Protein; 210 AA.
XX AC
XX AAB69103;
XX DT 23-APR-2001 (first entry)
XX DE Cedar pollen allergen T cell epitope derived protein SEQ ID NO:12.
XX KM Japanese cedar; Cryptomeria japonica; cedar pollen allergen;
XX KM T cell epitope; antisuigipollinosis.
XX OS
XX Cryptomeria japonica.
XX OS Synthetic.
XX PN JP2000327699-A.
XX PD 28-NOV-2000.
XX PF 15-MAR-2000; 2000JP-0071710.
XX PR 15-MAR-1999; 99JP-0068316.
XX PA (HAYB ) HAYASHIBARA SETIBUTSU KAGAKU.
XX PA (SANTY ) SANKYO CO LTD.
XX DR WPI; 2001-185061/19.
XX DR N-PSDB; AAF59012.

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XX Novel peptide and its use -
 PT
 XX
 PS Claim 7, Page 39-40; 75pp; Japanese.
 CC
 CC The present invention describes a peptide, its complex, derivative or
 CC its polymerizate, where the peptide (I) has a formula of:
 CC alpha1-alpha2-alpha3-alpha4-alpha5-alpha6-alpha7
 CC where alpha1 to alpha7 = amino acid sequence selected from amino acid
 CC sequences ranging from 11-19 amino acids derived from T cell epitopes
 CC derived from cedar (Japanese cedar - Cryptomeria japonica) pollen
 CC allergens. The peptide can be used in an antisugipollinosis agent.
 CC AAF59011 to AAF59062 and AAB69094 to AAB69121 represent sequences used
 CC in the exemplification of the present invention.
 XX

Sequence 210 AA;

Query Match 25.0%; Score 178; DB 22; Length 210;
 Best Local Similarity 32.5%; Pred. No. 3e-14; Mismatches 7; Indels 96; Gaps 6;
 Matches 53; Conservative 7; Mismatches 7; Indels 96; Gaps 6;

QY 1 MKYTVAFNQGPRKRVFIKRVSNVITHRRIDIFASKNFHLQKNT-IGTGR----- 50
 Db 29 MKYTVAFNQGPR-----FASKNFHLQKNTKLTSGKIASCLANYGL 67
 QY 51 -----RWKNNRIWL-----QFAKLTGFTLMGRRLMIFSGNNMIKLMKP 90
 Db 68 VHVANNNTDPSGKIEGNNITYTKEAFNVEQFAKLTGFTLMGRA----- 110
 QY 91 MYIAGYKTFDGRRAEVSYYVHNGAKFIRRVDSIIAAYONPASM 133
 Db 111 -----DPR-----GIIAAYONPASM 125

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 Job time : 47 secs

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Query Match 8.7%; Score 62; DB 9; Length 545;
 Best Local Similarity 25.7%; Pred. No. 47;
 Matches 29; Conservative 11; Mismatches 49; Indels 24; Gaps 6;

QY 45 TTGTRKNNRIMLOPAKL-----TGFRRLTIFSGNNN---IK 86

DB 29 SFGTGS-SNPSVGLNFGNLGTSPTATTSADSSGFGTLPFSKPAATGTTGCTNIGALH 87
 QY 87 LKMPYIAGYKTFDGRRAEVSYVHN---GAKFIRVDGII--AAAYNPASWK 134
 DB 88 TKRPQVTVTKYGTIGQKQMHVGTPIQVFLGVFSPRPPLGLRFAPEPPEPMK 140

RESULT 15
 US-10-174-590-58
 Sequence 58, Application US/10174590
 Publication No. US20030008352A1
 GENERAL INFORMATION:
 APPLICANT: Baker, Kevin P.
 APPLICANT: Chen, Jian
 APPLICANT: Desnoyers, Luc
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Garney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin

TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3430R1C42
 CURRENT APPLICATION NUMBER: US/10/174,590
 CURRENT FILING DATE: 2002-06-18
 Prior application removed - See File Wrapper or Palm
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 58
 LENGTH: 545
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-174-590-58

Query Match 8.7%; Score 62; DB 9; Length 545;
 Best Local Similarity 25.7%; Pred. No. 47;
 Matches 29; Conservative 11; Mismatches 49; Indels 24; Gaps 6;

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DB 88 TKRPQVTKYGTGLQGMHVKGKTPIOVFLGVFPSPRPPLGILRPAPEPEPEPWK 140

RESULT 14
US-09-978-189-254
Sequence 254, Application US/09978189
Publication No. US20030004102A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Geber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gueney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C7
CURRENT APPLICATION NUMBER: US/09/978,189
CURRENT FILING DATE: 2001-10-15
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 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697

Query Match 8.7%; Score 62; DB 9; Length 545;
 Best Local Similarity 25.7%; Pred. No. 47;
 Matches 29; Conservative 11; Mismatches 49; Indels 24; Gaps 6;

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PRIOR APPLICATION NUMBER:	60/085580
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PRIOR APPLICATION NUMBER:	60/085573
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085704
PRIOR FILING DATE:	1998-05-15
PRIOR APPLICATION NUMBER:	60/085697

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Query Match 8.7% Score 62; DB 9; Length 545;
Best Local Similarity 25.7%; Pred. No. 47;
Matches 29; Conservative 11; Mismatches 49; Indels 24; Gaps 6;

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DB       29 SEGTGTS-SNPESVGINFGNLGSTSPATTAPSAGFGGLFSKPKDATGFTLLGGTTGALH 87
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Db       88 TRRPOVVTVTYGLQGKQMVGCKTPIQVLGVPSRPDLGIILFPAPPPEPWK 140

RESULT 13
US-09-999-832A-254
Sequence 254, Application US/09999832A
Publication No. US20020192706A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoysers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Garber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gunney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William T.
TITLE OR INVENTION: Acids and Transmembrane Polypeptides and Nucleic
TITLE OR INVENTION: Acids Encoding the Same
FILE REFERENCE: P2630P1C63
CURRENT APPLICATION NUMBER: US/09/999,832A
CURRENT FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/064249
PRIOR FILING DATE: 1997-11-03
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/066364
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PRIOR APPLICATION NUMBER: 60/077450
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PRIOR APPLICATION NUMBER: 60/077632
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PRIOR APPLICATION NUMBER: 60/077641
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PRIOR APPLICATION NUMBER: 60/077649
PRIOR FILING DATE: 1998-03-11
PRIOR APPLICATION NUMBER: 60/077791
PRIOR FILING DATE: 1998-03-12
PRIOR APPLICATION NUMBER: 60/078004
PRIOR FILING DATE: 1998-03-13
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;; PRIOR FILING DATE: 1998-05-15
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Query Match 8.7%; Score 62; DB 9; Length 545;
Best Local Similarity 25.7%; Pred. No. 47;
Matches 29; Conservative 11; Mismatches 49; Indels 24; Gaps 6;
QY 45 TIGTGRMKNRIMIQFAKL-----TGF--TIMGRRPLMIFSGNMN---IK 86
DB 29 SFGTGS-SNPSVGLNFNGLSTSTPATTSAPSSGFGTGLFSGKATGFTLGGTNGALH 87
QY 87 LKHPMTIAGKTGDRRAEVSIVHVN---GAKIRRVDTIT--AAYONASMK 134
DB 88 TKRPQVVTXKGLQKQMHVGTKPIQVFLGVFPSPRLGLRLFAPEPPEPWK 140
RESULT 12
US-09-978-192A-254
; Sequence 254, Application US/09978192A
; Patent No. US20020177553A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi
; APPLICANT: Baker Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Baton, Dan
; APPLICANT: Ferrara, Napoleon
; APPLICANT: Filvaroff, Ellen
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; APPLICANT: Gao, Wei-Qiang
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; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Kljavin, Ivar J.
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; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James;
; APPLICANT: Paoni, Nicholas F.
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; APPLICANT: Shelton, David L.
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2630PLC9
; CURRENT APPLICATION NUMBER: US/09/978,192A
; PRIOR FILING DATE: 2001-10-15
; PRIOR APPLICATION NUMBER: 09/918585
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PRIOR APPLICATION NUMBER: 60/085573
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085704
 PRIOR FILING DATE: 1998-05-15
 PRIOR APPLICATION NUMBER: 60/085697
 Query Match 8.7%; Score 62; DB 9; Length 545;
 Best Local Similarity 25.7%; Pred. No. 47;
 Matches 29; Conservative 11; Mismatches 49; Indels 24; Gaps 6;
 QY 45 TGTGRKKNNRIWLOPAK-----TGF--TLMGRPLMIIFSGNN---IK 86
 Db 29 SFGTGS-SNPVNLNGNLSTPATTSAPSSGFGTGLFGSKPATGFTLGGTNGALH 87
 QY 87 LKMPMYAGYKTPDGRRAEYSYHVN---GAKIRAVDGI--AAQNPASWK 134
 Db 88 TKRPQVTKYKTLQGMHVKTPIOVFLGVPRSPPLGLRPAPEPPEPWK 140
 RESULT 11
 US-09-978-697-254
 Sequence 254, Application US/09978697
 Patent No. US20020169284A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi
 APPLICANT: Baker Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan
 APPLICANT: Ferrara, Napoleon
 APPLICANT: Filvaroff, Ellen
 APPLICANT: Fong, Sherman
 APPLICANT: Gao, Wei-Qiang
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gerritsen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Hillan, Kenneth J.
 APPLICANT: Kijavlin, Ivar J.
 APPLICANT: Kuo, Sophia S.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Peoni, Nicholas F.
 APPLICANT: Roy, Margaret Ann
 APPLICANT: Shelton, David L.
 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
 FILE REFERENCE: P2630PIC27
 CURRENT APPLICATION NUMBER: US/09/978,697
 PRIOR APPLICATION NUMBER: 09/918585
 PRIOR FILING DATE: 2001-10-16
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/064249
 PRIOR FILING DATE: 1997-11-03
 PRIOR APPLICATION NUMBER: 60/065311
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 PRIOR FILING DATE: 1997-11-21
 PRIOR APPLICATION NUMBER: 60/077450
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 PRIOR APPLICATION NUMBER: 60/077632
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077641
 PRIOR FILING DATE: 1998-03-11
 PRIOR APPLICATION NUMBER: 60/077649

LENGTH: 1375
TYPE: PRT
ORGANISM: streptococcus mutans
US-09-740-274-4

Query Match 8.8%; Score 62.5; DB 10; Length 1375;
Best Local Similarity 24.8%; Pred. No. 1.3e+02;
Matches 34; Conservative 17; Mismatches 53; Indels 33; Gaps 8;

Qy 10 FGNBVF---IKRVNVIHGRRIDIFASKNPHLOKNTIGG-----REKKNRIWL 59
Db 1185 FGGQWRYFONGIWAAGLTRYHG-AVOYFASGFGQAKGQITTTADGKLRFDSDGQISN 1243
Qy 60 QFAKLTGFTLMGRPLMIIFSGNMNIKLMPIYIAGYKTFDGRRAEVSYVNG-----AK 115
Db 1244 RFR-----NSKGMFLFDNH-----GVAVTGTVTFNQRL---YFKNGVQAGE 1286
Qy 116 FIRVDGIITAYONPAS 132
Db 1287 FIRDANGYL-RYYDPNS 1302

RESULT 10
US-09-978-295A-254
Sequence 254, Application US/09978295A
Patent No. US2002015606A1
GENERAL INFORMATION:
APPLICANT: Aekhenazi, Avi
APPLICANT: Baker Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleon
APPLICANT: Filvaroff, Ellen
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Kuo, Sophia S.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James;
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Shelton, David L.
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2630P1C11
CURRENT APPLICATION NUMBER: US/09/978,295A
CURRENT FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: 09/918585
PRIOR FILING DATE: 2001-07-30
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081838
PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/082568

GENERAL INFORMATION:
APPLICANT: Zuker, Charles S.
APPLICANT: Adler, Jon Elliot
APPLICANT: Ryba, Nick
APPLICANT: Mueller, Ken
APPLICANT: Hoon, Mark
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: T2R, a No. US20030022278a1el Family of Taste Receptors
FILE REFERENCE: 023078-098010US
CURRENT APPLICATION NUMBER: US/09/510,332
CURRENT FILING DATE: 2000-02-22
PRIOR APPLICATION NUMBER: US 09/393,634
PRIOR FILING DATE: 1999-09-10
NUMBER OF SEQ ID NOS: 172
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 85
LENGTH: 309
TYPE: PRT
ORGANISM: Rattus sp.
FEATURE:
OTHER INFORMATION: rat T2R05 (rGR05)
US-09-510-332-85

Query Match
Best Local Similarity 8.9%; Score 63; DB 9; Length 309;
Best Local Similarity 28.4%; Pred. No. 18;
Matches 23; Conservative 15; Mismatches 33; Indels 10; Gaps 4;

QY 52 WKNRRLWLPQAKLTGFTLMGRPLMIIFSGNNMIKL---KMPYIAGYTPGRRAE--V 106
DB 121 WLRRIIVFAFLIGLILMS---W-LFSFPVVXKVKOKMLYINSSQIMKSELI 175
QY 107 SYVHVGAKFIRRVGGIIAY 127
DB 176 NYFTNGVFLFIIMLIYCF 196

RESULT 5
US-08-915-048A-2
Sequence 2, Application US/08915048A
Patent No. US20020025569A1
GENERAL INFORMATION:
APPLICANT: Caliguri, Maureen
APPLICANT: Rolfe, Mark
TITLE OF INVENTION: Components of Ubiquitin Ligase Complexes
TITLE OF INVENTION: and Uses Related Thereto
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley, Hoag & Eliot
STREET: One Post Office Square
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII (text)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,048A
FILING DATE: 20-AUG-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Vincent, Matthew P.
REGISTRATION NUMBER: 36,709
REFERENCE/DOCKET NUMBER: MIV-092.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 832-1000
TELEFAX: (617) 832-7000
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1121 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-08-915-048A-2

Query Match
Best Local Similarity 8.9%; Score 63; DB 8; Length 1121;
Best Local Similarity 25.2%; Pred. No. 86;
Matches 26; Conservative 14; Mismatches 23; Indels 40; Gaps 6;

QY 10 FGPFRVFTIRGVNV---IIHGR-----IDIFASKNPHLQKXITGTGR 51
DB 46 FGHLEW-IRKVNGLGHYIHGFVRPEPNDLDEAMVAVSGKLRVVKISGQGHF 104
QY 52 WK-----NNRIWLPQAKLTGFTLMGRPLMIIFSGNNMIKL 87
DB 105 WELMRSGLMMSDWIMDAR-----WL--EGNIALAL 133

RESULT 6
US-10-114-893-73
Sequence 73, Application US/10114893
Publication No. US20020193567A1
GENERAL INFORMATION:
APPLICANT: Jacobs, Kenneth
APPLICANT: McCoy, John M.
APPLICANT: Lavallee, Edward R.
APPLICANT: Collins-Racie, Lisa A.
APPLICANT: Evans, Cheryl
APPLICANT: Werberg, David
APPLICANT: Treacy, Maurice
APPLICANT: Bowman, Michael R.
APPLICANT: Spaulding, Vikki
APPLICANT: Carlin-Duckett, McKeough
APPLICANT: Kelleher, Kerry S.
APPLICANT: Genetics Institute, Inc.
TITLE OF INVENTION: SECRETED PROTEINS AND POLYNUCLEOTIDES ENCODING THEM
FILE REFERENCE: GI 6000-10A
CURRENT APPLICATION NUMBER: US/10/114,893
CURRENT FILING DATE: 2002-04-02
EARLIER APPLICATION NUMBER: 09/413,232
EARLIER FILING DATE: 1999-10-06
NUMBER OF SEQ ID NOS: 321
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 73
LENGTH: 380
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: UNSURE
LOCATION: (135)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (179)
FEATURE:
NAME/KEY: UNSURE
LOCATION: (318)
US-10-114-893-73

Query Match
Best Local Similarity 8.8%; Score 62.5; DB 9; Length 380;
Best Local Similarity 27.4%; Pred. No. 26;
Matches 20; Conservative 14; Mismatches 32; Indels 7; Gaps 3;

QY 52 WKN--NNRIWLPQAKLTGFTLMGRPLMIIFSGNNMIKLKMPYIA--GYKTPDGRRAEVS 107
DB 257 WKNCCNNIFIVFAIVFPIITRLVILPFWIL--HCTIVPELIPAFPGYIFPNSMGVLQ 313
QY 108 YVHVGAKFIRRV 120
DB 314 LKHIXWAVLILRM 326

RESULT 7

```

; TELEPHONE: (415) 705-8410
; TELEFAX: (415) 397-8338
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
;     LENGTH: 2710 amino acids
;     TYPE: amino acid
;     TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-011-366-6

Query Match          10.0%; Score 71; DB 9; Length 2710;
Best Local Similarity 21.7%; Pred. No. 29;
Matches      36; Conservative    22; Mismatches   64; Indels    44; Gaps       7;

QY      3 VTVAENQGNRRVFIKVSNTIHGRRIDIPASKNFHLQKNITGTGRMKNRRIWIOFA 62
        :|::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      2256 ITIERNNFYFDANNESKNVTGVFGKPNGEFEYFAPANTH--NINIEGQAIVYONKFLLNGK 2314
        ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      63 K-----TLGF-TLMGRRPLMIIFSGNN-----IKLKMPTIAG 95
        :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      2315 KYFPNDSKAVTGMOTIDGK----YFPNLMTAEATGMOTIDGKKYFPLNTAAEATG 2369
        ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      96 YKTFDGR-----AEVSVYHVNGAKFIRVDGI--IAAYNP 130
        ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      2370 WQTIDGKYFENTNTFTASTGYTSINGHFYFNPDGIMQIGVFKEP 2415
        ::||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 3
US-09-393-634-9
; Sequence 9, Application US/09393634
; Patent No. US20020051997A1
; GENERAL INFORMATION:
; APPLICANT: Zuker, Charles S.
; APPLICANT: Adler, Jon Elliott
; APPLICANT: Ryda, Nick
; APPLICANT: Mueller, Ken
; APPLICANT: Hoon, Mark
; APPLICANT: The Regents of the University of California
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: SF, a No. US2002005197A1el Family of Taste Receptors
; FILE REFERENCE: 02307E-098000US
; CURRENT APPLICATION NUMBER: US/09/393,634
; CURRENT FILING DATE: 1999-09-10
; NUMBER OF SEQ ID NOS: 92
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 9
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Rattus sp.
; FEATURE:
; OTHER INFORMATION: rat GR05
US-09-393-634-9

Query Match          9.0%; Score 64; DB 10; Length 224;
Best Local Similarity 28.4%; Pred. No. 9.2;
Matches      23; Conservative    15; Mismatches   33; Indels    10; Gaps       4;

QY      52 WKNNRIWQFAKLGLFTLMGRRLPMIIFSGMMNIKL--KMPMTIAGKTPTDGRAE--V 106
        ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      121 WLKRINIVVPFLILGCLIMS---W-LFSPPVVAKVKDKMKLYNSWQTHMKSELI 175
        ||::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY      107 SYVHVNGAKFIRVDGI IAAV 127
        :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
DB      176 NYVFTNGGVFLFIHWIGCF 196
        :|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 4
US-09-510-332-85
; Sequence 85, Application US/09510332
; Publication No. US20030022278A1
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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 5, 2003, 16:59:07 ; Search time 46 Seconds

(without alignments)
251.357 Million cell updates/sec

Title: US-09-142-524d-3

Perfect score: 711

Sequence: 1 MKVTVAFNQFGPNRRVFIKR.....KFIKRVGIIIAAYGNPASMK 134

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 328255 seqs, 86286685 residues

Total number of hits satisfying chosen parameters: 328255

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubpaa/US08_NEM_PUB pep:*\n2: /cgn2_6/ptodata/2/pubpaa/PCT_NEM_PUB pep:*\n3: /cgn2_6/ptodata/2/pubpaa/US05_NEM_PUB pep:*\n4: /cgn2_6/ptodata/2/pubpaa/US06_NEM_PUB pep:*\n5: /cgn2_6/ptodata/2/pubpaa/US07_NEM_PUB pep:*\n6: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB pep:*\n7: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB pep:*\n8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB pep:*\n9: /cgn2_6/ptodata/2/pubpaa/US09_NEM_PUB pep:*\n10: /cgn2_6/ptodata/2/pubpaa/US09_PUBCOMB pep:*\n11: /cgn2_6/ptodata/2/pubpaa/US10_NEM_PUB pep:*\n12: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB pep:*\n13: /cgn2_6/ptodata/2/pubpaa/US60_NEM_PUB pep:*\n14: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	71	10.0	811	9	US-10-011-366-7
2	71	10.0	2710	9	US-10-011-366-6
3	64	9.0	224	10	US-09-393-634-9
4	63	8.9	309	9	US-09-510-332-85
5	63	8.9	1121	8	US-08-915-046A-2
6	62.5	8.8	380	9	US-10-114-893-73
7	62.5	8.8	481	9	US-10-121-032-15
8	62.5	8.8	481	9	US-10-093-037-15
9	62.5	8.8	1375	10	US-09-740-274-4
10	62	8.7	545	9	US-09-978-295A-254
11	62	8.7	545	9	US-09-978-697-254
12	62	8.7	545	9	US-09-978-192A-254
13	62	8.7	545	9	US-09-999-832A-254
14	62	8.7	545	9	US-09-978-189-254
15	62	8.7	545	9	US-10-174-590-58
16	62	8.7	545	9	US-10-176-758-58
17	62	8.7	545	9	US-10-175-737-58
18	62	8.7	545	9	US-10-173-706-58
19	62	8.7	545	9	US-10-175-738-58

20	62	8.7	545	9	US-10-175-752-58
21	62	8.7	545	9	US-10-176-482-58
22	62	8.7	545	9	US-10-176-757-58
23	62	8.7	545	9	US-10-176-913-58
24	62	8.7	545	9	US-10-180-552-58
25	62	8.7	545	9	US-10-180-557-58
26	62	8.7	545	9	US-10-174-572-58
27	62	8.7	545	9	US-10-174-572-58
28	62	8.7	545	9	US-10-174-587-58
29	62	8.7	545	9	US-10-174-587-58
30	62	8.7	545	9	US-10-174-588-58
31	62	8.7	545	9	US-10-173-739-58
32	62	8.7	545	9	US-10-175-740-58
33	62	8.7	545	9	US-10-175-743-58
34	62	8.7	545	9	US-10-176-488-58
35	62	8.7	545	9	US-10-176-492-58
36	62	8.7	545	9	US-10-176-747-58
37	62	8.7	545	9	US-10-176-750-58
38	62	8.7	545	9	US-10-176-985-58
39	62	8.7	545	9	US-10-176-987-58
40	62	8.7	545	9	US-10-176-991-58
41	62	8.7	545	9	US-10-176-992-58
42	62	8.7	545	9	US-10-176-993-58
43	62	8.7	545	9	US-10-184-658-58
44	62	8.7	545	9	US-10-173-695-58
45	62	8.7	545	9	US-10-173-697-58

ALIGNMENTS

RESULT 1
US-10-011-366-7
Sequence 7, Appli
Publication No. US20030054493A1
GENERAL INFORMATION:
APPLICANT: Williams, James A.
Kink, John A.
TITLE OF INVENTION: IDENTIFICATION OF NEUTRALIZING EPITOPES
OF TOXIN A AND TOXIN B FOR THE TREATMENT OF C. DIFFICILE
DISEASE
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: Medlen & Carroll
STREET: 220 Montgomery Street, Suite 2200
City: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/011,366
FILING DATE: 16-NO. US20030054493A1-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/957,310
FILING DATE: 23-OCT-1997
APPLICATION NUMBER: US 08/329,154
FILING DATE: 24-OCT-1994
APPLICATION NUMBER: US 08/161,907
FILING DATE: 02-DEC-1993
APPLICATION NUMBER: US 07/985,321
FILING DATE: 04-DEC-1992
APPLICATION NUMBER: US 07/429,791
FILING DATE: 31-OCT-1989
ATTORNEY/AGENT INFORMATION:
NAME: Ingolia, Diane E.
REGISTRATION NUMBER: 40,027
REFERENCE/DOCKET NUMBER: OPHD-01121

GenCore version 5.1.4.p5.4578
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OM protein - protein search, using sw model

Run on: April 20, 2003, 12:56:55 ; Search time 12.6711 Seconds
(without alignments)
243.919 Million cell updates/sec

Title: US-09-142-524D-152

Perfect score: 67

Sequence: 1 LSDISLKTSGKIAS 15

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mmc:*
8: sp_organelle:*
9: sp_phage:*
10: sp_plant:*
11: sp_rodent:*
12: sp_virus:*
13: sp_vertebrate:*
14: sp_unclassified:*
15: sp_virus:*
16: sp_bacteriophage:*
17: sp_archaeal:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	51	76.1	507	10	Q9FY19
2	45	67.2	251	16	Q8Z5M6
3	45	67.2	268	16	Q8Z5M6
4	44	65.7	242	16	Q8Z5M6
5	43	64.2	275	16	Q9KKE1
6	43	64.2	275	16	Q9KKE1
7	42	62.7	261	2	Q9R6G1
8	42	62.7	1376	3	Q8X1P2
9	40	59.7	134	16	Q8UDM0
10	40	59.7	253	16	Q8Z5M6
11	40	59.7	264	16	Q8Z5M6
12	40	59.7	278	9	Q8SCM6
13	40	59.7	299	16	Q9R6G1
14	40	59.7	299	16	Q9R6G1
15	40	59.7	317	3	Q8UDM0
16	40	59.7	1066	4	Q96DN5

17	39	58.2	93	16	Q9K9U3
18	39	58.2	225	2	Q9AH14
19	39	58.2	292	16	Q8Z5M6
20	39	58.2	292	16	Q8Z5M6
21	39	58.2	325	10	Q9S219
22	39	58.2	393	16	Q8S461
23	39	58.2	649	10	Q9W1C1
24	39	58.2	839	10	Q9W1C1
25	39	58.2	1446	10	Q9S219
26	38	56.7	226	16	Q9S219
27	38	56.7	226	16	Q9S219
28	38	56.7	230	16	Q9S219
29	38	56.7	241	16	Q9S219
30	38	56.7	251	16	Q9S219
31	38	56.7	257	16	Q9S219
32	38	56.7	273	16	Q9S219
33	38	56.7	291	16	Q9S219
34	38	56.7	291	16	Q9S219
35	38	56.7	359	13	Q9S219
36	38	56.7	398	10	Q9S219
37	38	56.7	475	16	Q9S219
38	38	56.7	505	16	Q9S219
39	38	56.7	529	12	Q9S219
40	38	56.7	548	10	Q9S219
41	38	56.7	568	16	Q9S219
42	37.5	56.0	1167	12	Q9S219
43	37	55.2	124	16	Q9S219
44	37	55.2	165	16	Q9S219
45	37	55.2	194	2	Q9K170

ALIGNMENTS

RESULT 1
Q9FY19 PRELIMINARY; PRT; 507 AA.
ID Q9FY19
AC Q9FY19
DT 01-MAR-2001 (TREMELREL. 16, Created)
DT 01-MAR-2001 (TREMELREL. 16, Last sequence update)
DT 01-JUN-2002 (TREMELREL. 21, Last annotation update)
DE Pollen major allergen 2 protein precursor.
GN JNA2.
OS Juniperus ashei (Ozark white cedar).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Cupressaceae; Juniperus.
OX NCBI_TaxID=13101;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=MALE POLLEN;
RX MEDLINE=20403896; PubMed=10944464;
RA Yokoyama M., Miyahara M., Shimizu K., Kino K., Tsunoo H.;
RT Purification, identification and cDNA cloning of Jun a 2, the second
RT major allergen of mountain cedar pollen."
RL Biochem. Biophys. Res. Commun. 275:195-202(2000).
CC -1- SIMILARITY: BELONGS TO FAMILY 28 OF GLYCOSYL HYDROLASES
(POLYGALACTURONASES).
CC EMBL: AJ040463; CAC05582.1; --
DR HSSP; P26509; IBB.
DR InterPro; IPR000743; GH28.
DR InterPro; IPR000408; Reg. chr. condens.
DR Pfam; PF00295; Glyco_hydro_28; 1.
DR PROSITE; PS00502; POLYGALACTURONASE; UNKNOWN_1.
DR PROSITE; PS00626; RCCL_2; UNKNOWN_1.
KW Cell wall; Glycosidase; Hydrolyase; Signal.
FT SIGNAL
SQ SEQUENCE 507 AA; 55730 MW; 2B2E0AA5E958FE5A CRC64;
Query Match 76.1%; Score 51; DB 10; Length 507;
Best Local Similarity 66.7%; Pred. No. 0.58;
Matches 10; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
QY 1 LSDISLKTSGKIAS 15

Db 396 LSNDVSLKTSKXAT 410

RESULT 2

Q825W6 PRELIMINARY; PRT; 251 AA.

AC Q825W6;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 21, Last annotation update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE High-affinity zinc uptake system ATP-binding protein.

GN STY2100.

OS Salmonella typhi.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Salmonella.

OK NCBI_Taxid=601;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CT18;

RX MEDLINE=21534947; PubMed=11677608;

RA Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Main J.,

RA Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahia M.,

RA Baker S., Basham D., Brooks K., Chillingworth T., Connor P.,

RA Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

RA Feltham T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,

RA Krogan A., Larsen T.S., Leather S., Moule S., O'Garra P., Parry C.,

RA Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,

RA Whitehead S., Barrett B.G.,

RT "Complete genome sequence of a multiple drug resistant Salmonella

RT enterica serovar Typh CT18."

RL Nature 413:848-852 (2001).

DR EMBL; AL627272; CAD05643.1; -

DR InterPro: IPR003593; AAA_ATPase.

DR InterPro: IPR003439; ABC_transport.

DR Pfam; PF00005; ABC_tran; 1.

DR ProDom; PD000006; ABC_transport; 1.

DR SMART; SM00382; AAA; 1.

DR ATP-binding; Complete proteome.

KW SEQUENCE 251 AA; 27731 MW; 4099397813CBBB0 CRC64;

SO

Query Match 67.2%; Score 45; DB 16; Length 251;

Best Local Similarity 69.2%; Pred. No. 3.7;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LSDISLKTSGKI 13

Db 20 LSDVSLKTSKXAT 32

RESULT 3

Q825W6 PRELIMINARY; PRT; 268 AA.

AC Q825W6;

DT 01-MAR-2002 (TrEMBLrel. 20, Created)

DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE ABC superfamily (atp_bind) high affinity Zn transport protein.

GN ZNUC OR STM189.

OS Salmonella typhimurium.

OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;

OC Salmonella.

OK NCBI_Taxid=602;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=LT2 / SSGC1412 / ATCC 700720;

RX MEDLINE=21534948; PubMed=11677609;

RA McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P.,

RA Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D.,

RA Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E.,

RA Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,

RA Waterston R., Wilson R.K.;

"Complete genome sequence of Salmonella enterica serovar Typhimurium

RT LT2."

RL Nature 413:852-856 (2001).

DR EMBL; AE008784; AAL20808.1; -

DR InterPro: IPR003593; AAA_ATPase.

DR InterPro: IPR003439; ABC_transport.

DR Pfam; PF00005; ABC_tran; 1.

DR ProDom; PD000006; ABC_transport; 1.

DR SMART; SM00382; AAA; 1.

KW Complete proteome.

SO SEQUENCE 268 AA; 29750 MW; D5669D2448A74B28 CRC64;

Query Match 67.2%; Score 45; DB 16; Length 268;

Best Local Similarity 69.2%; Pred. No. 4;

Matches 9; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 LSDISLKTSGKI 13

Db 37 LSDVSLKTSKXAT 49

RESULT 4

Q97N70 PRELIMINARY; PRT; 242 AA.

AC Q97N70;

DT 01-OCT-2001 (TrEMBLrel. 18, Created)

DT 01-OCT-2001 (TrEMBLrel. 18, Last sequence update)

DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)

DE ABC transporter, ATP-binding protein.

GN SP2196.

OS Streptococcus pneumoniae.

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;

OC Streptococcaceae; Streptococcus.

OK NCBI_Taxid=1313;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=TIGR4;

RX MEDLINE=21357209; PubMed=11463916;

RA Tettelin H., Nelson K.E., Paulsen I.T., Eisen J.A., Read T.D.,

RA Peterson S., Heidelberg J., DeBoy R.T., Haft D.H., Dodson R.J.,

RA Durkin A.S., Gwinn M., Kolonay J.F., Nelson W.C., Peterson J.D.,

RA Umayam L.A., White O., Salzberg S.L., Lewis M.R., Radune D.,

RA Holtzapple E., Khouri H., Wolf A.M., Utterback T.R., Hansen C.L.,

RA McDonald L.A., Feldblyum T.V., Angiuoli S., Dickinson T., Hickey E.K.,

RA Holt I.E., Loftus B.J., Yang F., Smith H.O., Venter J.C.,

RA Dougherty B.A., Morrison D.A., Hollingshead S.K., Fraser C.M.;

RT "Complete genome sequence of a virulent isolate of Streptococcus

RT pneumoniae."

RL Science 293:498-506 (2001).

DR EMBL; AE007508; AAK76247.1; -

DR TIGR; SP2196; -

DR InterPro: IPR003593; AAA_ATPase.

DR InterPro: IPR003439; ABC_transport.

DR InterPro: IPR001005; Myb_DNA_binding.

DR Pfam; PF00005; ABC_tran; 1.

DR SMART; SM00382; AAA; 1.

DR PROSITE; PS00211; ABC_TRANSPORTER; UNKNOWN_1.

DR PROSITE; PS00037; MYB_1; UNKNOWN_1.

KW ATP-binding; Complete proteome.

SO SEQUENCE 242 AA; 27519 MW; F88BD2FDD31DB35 CRC64;

Query Match 65.7%; Score 44; DB 16; Length 242;

Best Local Similarity 53.3%; Pred. No. 5.5;

Matches 8; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 LSDISLKTSGKIAS 15

Db 19 LEDINLDTSGEVS 33

RESULT 5

Q9KKE1 PRELIMINARY; PRT; 275 AA.

ID Q9KKE1

AC Q9KKE1;

DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Inner membrane ATPase protein (Histidine transport ATP-binding ABC transporter protein)
 GN HISV OR R02702 OR SMC00670.
 OC Rhizobium meliloti (Sinorhizobium meliloti).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Sinorhizobium.
 OC NCBI_TaxID=382;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RM5000;
 RX MEDLINE=20309701; PubMed=10850986;
 RA Boncompagni E., Dupont L., Mignot T., Osteras M., Lambert A.,
 RA Poggi M.-C., Le Rudulier D.;
 RT "Characterization of a Sinorhizobium meliloti ATP-Binding Cassette
 RT Histidine Transporter Also Involved in Betaine and Proline Uptake";
 RL J. Bacteriol. 182:3717-3725(2000).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAIN=1021;
 RC MEDLINE=21396507; PubMed=11481430;
 RA Capela D., Barloy-Hubler F., Guzy J., Bothe G., Ampe F., Batut J.,
 RA Boiteard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,
 RA Godie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masny D.,
 RA Pohl T., Portetle D., Puehler A., Purnelle B., Rampersingh U.,
 RA Renard C., Theault P., Vandenbol M., Weidner S., Galibert F.;
 RT "Analysis of the chromosome sequence of the legume symbiont
 RT Sinorhizobium meliloti strain 1021";
 RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL; AF111939; AAF78099.1; -;
 DR EMBL; AL591791; CAC47281.1; -;
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Transport; Complete proteome.
 SQ SEQUENCE 275 AA; 30364 MW; 99C41F56CF93790F CRC64;

Query Match 64.2%; Score 43; DB 16; Length 275;
 Best Local Similarity 61.5%; Pred. No. 9.6;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LSDISLKTSGKI 13
 ID 43 LNDVSLKIGAKI 55

RESULT 6
 Q9CKJ4 PRELIMINARY; PRT; 717 AA.
 AC Q9CKJ4;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE 14, 17 days embryo head cDNA, RIKEN full-length enriched library,
 DE clone:322401P09, full insert sequence (RIKEN cDNA 4833412N02
 DE gene).
 GN 4833412N02RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=EMBRYONIC HEAD;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Kawai T., Hara A., Fukumishi Y., Konno H., Adachi J., Fukuda S.,

RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Glasziou C., King B., Kochias H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schriml L.M., Staudl F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Guernich S., Hill D., Hofmann M., Hume D.A., Kamya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Wombardis P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata R., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 409:685-690(2001).
 [2]
 RN SEQUENCE FROM N.A.
 RP STRAUSBERG R.;
 RC TISSUE=KIDNEY;
 RA Submitted (Oct-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK014519; BAB29270.1; -;
 DR EMBL; BC015301; AAH15301.1; -;
 DR HSP; P13569; INBD.
 DR MGD; MG1:1921860; 4833412N02RIK.
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR001140; ABCTransporter.
 DR InterPro; IPR003439; ABC_transporter.
 DR Pfam; PF00664; ABC_membrane; 1.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transporter; 1.
 DR SMART; SM00382; AAA; 1.
 DR PROSITE; PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding.
 SQ SEQUENCE 717 AA; 77999 MW; E573D4276B9658EB CRC64;

Query Match 64.2%; Score 43; DB 11; Length 717;
 Best Local Similarity 60.0%; Pred. No. 25;
 Matches 9; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 LSDISLKTSGKIAS 15
 DB 472 LKDFTLKLPKGIKVA 486

RESULT 7
 Q9REG1 PRELIMINARY; PRT; 261 AA.
 ID Q9REG1;
 AC Q9REG1;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE TIORP98 protein.
 GN TIORP98.
 OS Agrobacterium tumefaciens.
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OC NCBI_TaxID=358;
 [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAF301001;
 RX MEDLINE=20184752; PubMed=10721727;
 RA Suzuki K., Hattori Y., Uraji M., Ohta N., Iwata K., Murata K.,
 RA Katoh A., Yoshida K.;
 RT "Complete nucleotide sequence of a plant tumor-inducing Ti plasmid";
 RL Gene 242:331-336(2000).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=MAF301001;
 RX MEDLINE=98193120; PubMed=9524202;

RA Suzuki K., Ohta N., Hattori Y., Uraji M., Katoh A., Yoshida K.;
 RT "Novel structural difference between nopaline- and octopine- type *trb*
 RT gene: construction of genetic and physical map and sequencing of
 RT *trb*/trb and rep gene clusters of a new *Tr* plasmid *pti*-SAKURA.",
 RL Biochim. Biophys. Acta 1396:1-7(1998).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF301001;
 RA Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;
 RT "Genome structure of *pti*-SAKURA (I): Strategy for DNA sequencing of a
 RT Japanese cherry-*Tr* plasmid."
 RL Nucleic Acids Symp. Ser. 37:159-160(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF301001;
 RA Ohta N., Suzuki K., Hattori Y., Uraji M., Katoh A., Yoshida K.;
 RT "Genome structure of *pti*-SAKURA (III): Characteristics of T-DNA."
 RL Nucleic Acids Symp. Ser. 39:185-186(1998).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF301001;
 RA Uraji M., Suzuki K., Ohta N., Hattori Y., Katoh A., Yoshida K.;
 RT "Genome structure of *pti*-SAKURA (IV): Characteristics of *tra* region."
 RL Nucleic Acids Symp. Ser. 39:187-188(1998).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MAFF301001;
 RA Hattori Y., Suzuki K., Ohta N., Uraji M., Katoh A., Yoshida K.;
 RT "Genome structure of *pti*-SAKURA (V): Complete nucleotide sequence of
 RT plasmid *pti*-SAKURA's *vir* region in *Agrobacterium tumefaciens*."
 RL Nucleic Acids Symp. Ser. 39:265-266(1998).
 DR EMBL: AB015260; RA87723.1; -
 DR InterPro: IPR003593; AAA_Atpase.
 DR InterPro: IPR003439; ABC_transport.
 DR Pfam: PF00005; ABC_tran; 1.
 DR ProDom: PD000006; ABC_transport; 1.
 DR SMART: SM00382; AAA; 1.
 KW ATP-binding; plasmid.
 SQ SEQUENCE 261 AA; 27971 MW; 451054F02082BF9B CRC64;
 QY Query Match 62.7%; Score 42; DB 2; Length 261;
 Best Local Similarity 61.5%; Pred. No. 14;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LSDISLKITSGKI 13
 DB 35 LSDVSLKAMAGKV 47
 RESULT 8
 ID 08X1P2 PRELIMINARY; PRT; 1376 AA.
 AC 08X1P2;
 DT 01-MAR-2002 (T-EMBLrel. 20, Created)
 DT 01-MAR-2002 (T-EMBLrel. 20, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Beta transducin-like protein HET-D2Y.
 GN HET-D.
 OS Podopora anserina.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariales; Lasiosphaeriaceae; Podospora.
 OX NCBI_TaxID=5145;
 RN RN
 RP SEQUENCE FROM N.A.
 RA Espagne B., Balhadere P., Begueret J., Turcq B.;
 RT "A new family of WD40 proteins implicated in vegetative
 RT incompatibility: evidence for a major role of WD40 repeat domain in
 RT the specificity of het-e and het-d genes."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF323585; AAL37301.1; -
 DR InterPro: IPR001680; WD40.
 DR Pfam: PF00400; WD40; 12.
 DR PRINTS: PR00320; GPROTEINBRPT.

DR ProDom: PD000018; WD40; 9.
 DR SMART: SM00320; WD40; 12.
 DR PROSITE: PS00678; WD_REPEATS_1; UNKNOWN_11.
 DR PROSITE: PS00682; WD_REPEATS_2; 11.
 DR PROSITE: PS50294; WD_REPEATS_REGION; 1.
 SQ SEQUENCE 1376 AA; 152068 MW; 2191826A562D97 CRC64;
 QY Query Match 62.7%; Score 42; DB 3; Length 1376;
 Best Local Similarity 69.2%; Pred. No. 73;
 Matches 9; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 1 LSDISLKITSGKI 13
 DB 643 ISDRSLKITSGKL 655
 RESULT 9
 ID 08UDM0 PRELIMINARY; PRT; 134 AA.
 AC 08UDM0;
 DT 01-JUN-2002 (T-EMBLrel. 21, Created)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Hypothetical protein At2g104.
 GN At2g104 OR AGR C 3816.
 OS *Agrobacterium tumefaciens* (strain C58 / ATCC 33970).
 OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
 OC Rhizobiaceae; Rhizobium.
 OX NCBI_TaxID=176299;
 RN RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608550; PubMed=11743193;
 RA Wood D.W., Serubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
 RA Ockura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F., Jr., Woo L.,
 RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D., Sr.,
 RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
 RA Kutayavin T., Levy R., Li M.-J., McEllelland E., Palmeri A.,
 RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
 RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
 RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
 RA Chumley F., Tingey S.V., Tomb J.-F., Gordon M.P., Olson M.V.,
 RA Nester E.W.;
 RT "The genome of the natural genetic engineer *Agrobacterium tumefaciens*
 RT C58."
 RL Science 294:2317-2323(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21608551; PubMed=11743194;
 RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M.,
 RA Ourriello B., Goldman B.S., Cao Y., Askenazi M., Halling C., Mullin L.,
 RA Houmlet K., Gordon J., Vaudin M., Iarchouk O., Epp A., Liu F.,
 RA Wollan C., Allinger M., Doughty D., Scott C., Lappe C., Markelz B.,
 RA Flanagan C., Crowell C., Gursen J., Lomo C., Sear C., Strub G.,
 RA Cielo C., Slater S.;
 RT "Genome sequence of the plant pathogen and biotechnology agent
 RT *Agrobacterium tumefaciens* C58."
 RL Science 294:2323-2328(2001).
 DR EMBL: AE009161; AAL43095.1; ALT_INT.
 DR EMBL: AE008127; AAK87853.1; -
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 134 AA; 14071 MW; EB868269D7DDP85 CRC64;
 QY Query Match 59.7%; Score 40; DB 16; Length 134;
 Best Local Similarity 40.0%; Pred. No. 17;
 Matches 6; Conservative 6; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LSDISLKITSGKIAS 15
 DB 99 MTDLKITSGNVAA 113
 RESULT 10
 08ZEU3

ID 08ZEU3 PRELIMINARY; PRT; 253 AA.
 AC 08ZEU3;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE High-affinity zinc uptake system ATP-binding protein.
 GN ZNOC OR YPO2060.
 OS Yersinia pestis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Yersinia.
 NCBI_TaxID=632;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CO-92 / BIOVAR ORIENTALIS;
 RX MEDLINE=21470413; PubMed=11586360;
 RA Parthill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
 RA Prentice M.B., Sebaldia M., James K.D., Churcher C., Mungall K.L.,
 RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
 RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
 RA Felwell T., Hamlin N., Holtroyd S., Jagers K., Karlyshev A.V.,
 RA Feltham S., Moulton S., Oyston P.C.F., Quail M., Rutherford K.,
 RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
 RT "Genome sequence of Yersinia pestis, the causative agent of plague."
 RL Nature 413:523-527(2001).
 DR EMBL; AJ414151; CAC90872.1; --
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transport.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transport; 1.
 DR SMART; SM00382; AAA; 1.
 KM ATP-binding; Complete proteome.
 SQ SEQUENCE 253 AA; 27620 MW; 15D202387927169B CRC64;

Query Match 59.7%; Score 40; DB 16; Length 253;
 Best Local Similarity 69.2%; Pred. No. 32;
 Matches 9; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 1 LSDISLKTSGKI 13
 Db 21 LSDISLKTSGKI 33

RESULT 11
 Q8RG16 PRELIMINARY; PRT; 264 AA.
 ID 08RG16;
 AC 08RG16;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Iron(III) dicitrate transport ATP-binding protein fcbB.
 GN FN0307.
 OS Fusobacterium nucleatum (subsp. nucleatum).
 OC Bacteria; Fusobacteria; Fusobacterium.
 NCBI_TaxID=76856;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=ATCC 25586;
 RX MEDLINE=21886394; PubMed=11889109;
 RA Bhattacharya A., Anderson I., Ivanova N., Reznik G., Los T., Lykidis A.,
 RA Vastava O., Chu L., Kogan Y., Chaga O., Goldstein E., Bernal A.,
 RA Lareen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
 RA Fontein M., Kyriides N., Overbeek R.;
 RT "Genome sequence and analysis of the oral bacterium Fusobacterium
 RT nucleatum strain ATCC 25586."
 RL J. Bacteriol 184:2005-2018(2002).
 DR EMBL; AF010543; AAL94513.1; --
 KM ATP-binding; Complete proteome.
 SQ SEQUENCE 264 AA; 30009 MW; 04C8BD94F121B53 CRC64;

Query Match 59.7%; Score 40; DB 16; Length 264;
 Best Local Similarity 61.5%; Pred. No. 33;
 Matches 8; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 LSDISLKTSGKI 13
 Db 22 LKDIINLKTSGKI 34

RESULT 12
 Q8SCM8 PRELIMINARY; PRT; 278 AA.
 ID 08SCM8;
 AC 08SCM8;
 DT 01-JUN-2002 (TREMBlrel. 21, Created)
 DT 01-JUN-2002 (TREMBlrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Pseudomonas phage phiKZ.
 OS Pseudomonas phage phiKZ.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae.
 NCBI_TaxID=169683;
 RX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21914557; PubMed=11916376;
 RA Mesyanzhinov V.V., Robben J., Grymonprez B., Kostyuchenko V.A.,
 RA Bourkatsava M.V., Sykylinda N.N., Krylov V.V., Volkasert G.;
 RT "The genome of bacteriophage phiKZ of Pseudomonas aeruginosa."
 RL J. Mol. Biol. 317:1-19(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Mesyanzhinov V.V., Robben J., Grymonprez B., Kostyuchenko V.A.,
 RA Bourkatsava M.V., Sykylinda N.N., Krylov V.V., Volkasert G.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF399011; AAL83185.1; --
 SQ SEQUENCE 278 AA; 31883 MW; C7A2CA9FDE57AD5A CRC64;

Query Match 59.7%; Score 40; DB 9; Length 278;
 Best Local Similarity 53.8%; Pred. No. 35;
 Matches 7; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
 Qy 3 DISLKTSGKIAS 15
 Db 220 DVLLKLTNGKYS 232

RESULT 13
 Q99RT2 PRELIMINARY; PRT; 299 AA.
 ID 099RT2;
 AC 099RT2;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Hypothetical protein SA2132.
 GN SA2132.
 OS Staphylococcus aureus (strain N315).
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Staphylococcus.
 NCBI_TaxID=158879;
 RX [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=2131952; PubMed=11418146;
 RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,
 RA Cui L., Oguchi A., Aoki K.I., Nagai Y., Ito T., Kanamori M.,
 RA Takamatsu H., Maruyama A., Murakami H., Hoshiyama A., Mizutani-Ui Y.,
 RA Takashashi N.K., Sawano T., Inoue R.I., Kaito C., Sekimizu K.,
 RA Hiraoka H., Kohara S., Goto S., Yabuzaki J., Kanehisa M.,
 RA Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T., Hattori M.,
 RA Ogasawara N., Hayashi H., Hiramoto K.;
 RT "Whole genome sequencing of methicillin-resistant Staphylococcus
 RT aureus."
 RL Lancet 357:1225-1240(2001).
 DR EMBL; AP003136; BAB43433.1; --
 DR InterPro; IPR003593; AAA_ATPase.
 DR InterPro; IPR003439; ABC_transport.
 DR Pfam; PF00005; ABC_tran; 1.
 DR ProDom; PD000006; ABC_transport; 1.
 DR SMART; SM00382; AAA; 1.

DR PROSITE: PS00211; ABC TRANSPORTER; UNKNOWN_1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 299 AA; 33723 MM; BABFECB011FFD7C CRC64;

Query Match 59.7%; Score 40; DB 16; Length 299;
 Best Local Similarity 61.5%; Pred. No. 37;
 Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LSDISLKLTSKGI 13
 ::|||:|
 DB 18 VNDISLELSGKM 30

RESULT 14

ID Q931F9 PRELIMINARY; PRT; 299 AA.

AC Q931F9; 01-DEC-2001 (TREMBlrel. 19, Created)

DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DE Hypothetical protein SAV2341.

GN SAV2341.

OS Staphylococcus aureus (strain Mu50 / ATCC 700639).

OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;

OX NCBI_Taxid=158878;

RN NCBI_Taxid=158878;

RP SEQUENCE FROM N.A.

RA MEDLINE=21311952; PubMed=11418146;

RA Kuroda M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

RA Cui L., Oguchi A., Aoki K.-I., Nagai Y., Lian J.-Q., Ito T.,

RA Kanamori M., Matsumaru H., Maruyama A., Murakami H., Hosoyama A.,

RA Mizutani-Uji Y., Takahashi N.K., Sawano T., Inoue R.-I., Kaiko C.,

RA Sekimizu K., Hirakawa H., Kuhara S., Goto S., Yabuzaki J.,

RA Kanehisa M., Yamashita A., Oshima K., Furuya K., Yoshino C., Shiba T.,

RA Hattori M., Ogasawara N., Hayashi H., Hiramatsu K.,

RT "Whole genome sequencing of methicillin-resistant Staphylococcus

RT aureus";

RL Lancet 357:1225-1240(2001).

DR EMBL; AP003365; BAB58503.1; -

DR InterPro; IPR003439; ABC_transporter.

DR Pfam; PF00005; ABC_tran; 1.

DR ProDom; PD000006; ABC_transporter; 1.

DR PROSITE: PS00211; ABC_TRANSPORTER; UNKNOWN_1.

KW Hypothetical protein; Complete proteome.

SQ SEQUENCE 299 AA; 33757 MM; 798FEC58F21FFD7A CRC64;

Query Match 59.7%; Score 40; DB 16; Length 299;

Best Local Similarity 61.5%; Pred. No. 37;

Matches 8; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 1 LSDISLKLTSKGI 13
 ::|||:|
 DB 18 VNDISLELSGKM 30

RESULT 15

ID Q9UDU9 PRELIMINARY; PRT; 317 AA.

AC Q9UDU9; 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE Hypothetical 37.0 kDa protein.

GN SPBC179.13C.

OS Schizosaccharomyces pombe (Fission Yeast).

OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;

OC Schizosaccharomycetales; Schizosaccharomycetaceae;

OC Schizosaccharomycetes.

OX NCBI_Taxid=4896;

RN NCBI_Taxid=4896;

RP SEQUENCE FROM N.A.

RC STRAIN=572H-;

RA Wood V., Rajandream M.A., Barrell B.G., Volskaert G.,

RL Submitted (Aug-1999) to the EMBL/Genbank/DBJ databases.

DR EMBL; AL109846; CAB52811.1; -

KW Hypothetical protein.

SQ SEQUENCE 317 AA; 37009 MM; C4356E2E97057126 CRC64;

Query Match 59.7%; Score 40; DB 3; Length 317;
 Best Local Similarity 61.5%; Pred. No. 40;
 Matches 8; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 LSDISLKLTSKGI 13
 |||||:|
 DB 297 LSDIQLRLNVGKV 309

Search completed: April 20, 2003, 13:13:23
 Job time : 14.6711 secs